

Figure 1

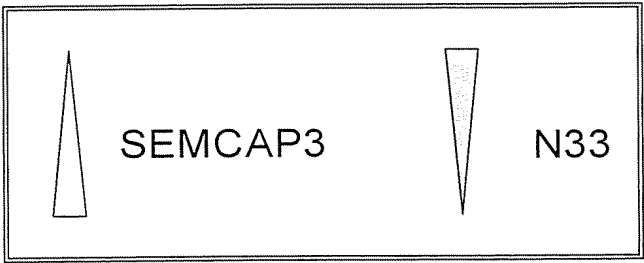
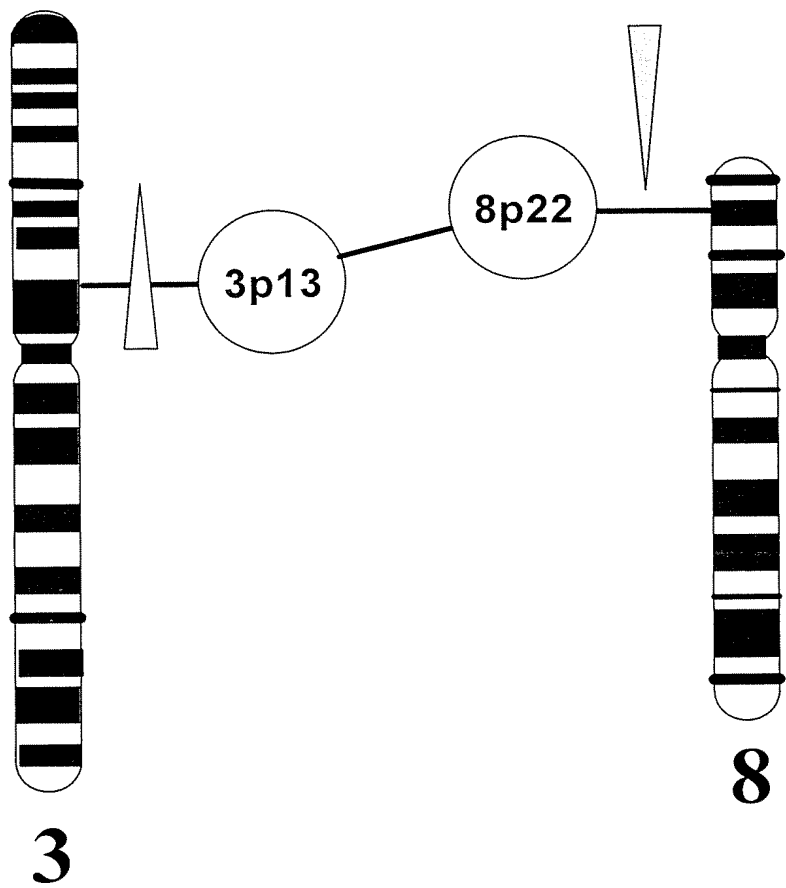
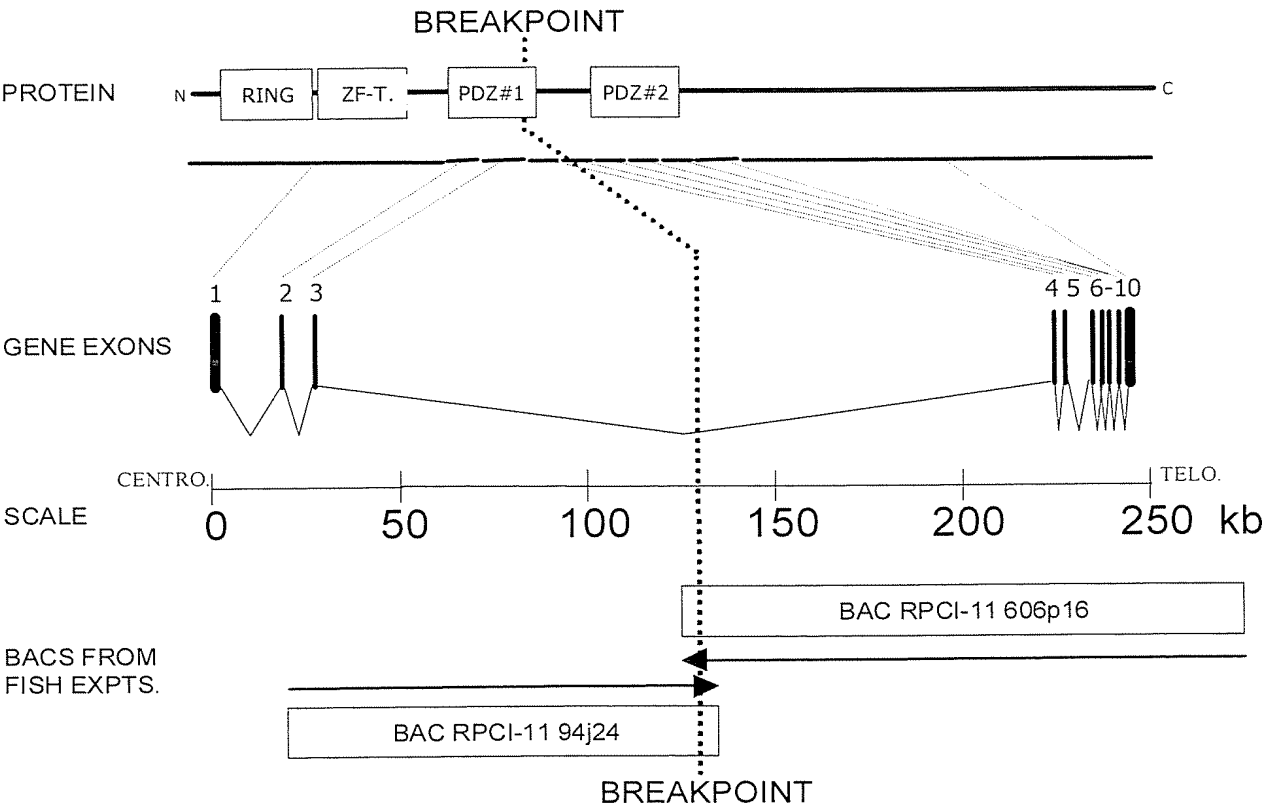


Figure 2



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Figure 3 (SEQ ID NO: 1)

1 AAAACTTCCC CGGGTAGATT CACCCACCGG TCCTGGAAAC CTGCTAAATC CTGAAGGTTC
61 ACAGAACCTC TGGTCAGAAC TGAAGTTGCA GCCGGAGCTT CCCGAGGCT CTGTAACTTT
121 CCCTGGAATG AAATAAATAA ATAAAGACCG TAAGTGCTGA GATAGCGGGC CCCAAGATAT
181 TTTTAGTCTT CTGCAATCAG CCACTAGAGG AAGGGGGAGG GAGAAGGGAG TAAAAAAGTT
241 TTGATCCGTT CGGGAAGGGG CTCGAAGAGA ACCCTTGGGA GAAAGCAGTA GCCTCAGCTC
301 CAAACTCAGC GAGCTTTTCT CGGCTGGCGT TTTGTCTCCT ATAGCGTAGA CTGTAAGAGA
361 ACAGAAAGGA GTTTCCCGAG AAGATTCAGG CTGGCGTCCT GGGCTGGCCC GTCCCTTCTG
421 GCGAGCCTCA GTGTCTCTCC ACGCGCTTCT GCCTTCCAGC CTCCTCCCTT TTTCGGGGGG
481 CTGGCGGGAG GCATCCAAGG CACGATGTAT GTGCGCTCGC GCTCGCGCAA ATACGGCCGG
541 AGGAGTCCTG TTCCTCGGGC ATTTTCCGAG GAAGTCTGGA TCAATTAGGC TCAGTCCGGG
601 GAGAGCCAGC GAGCGCGCGG GCGGCGTAGC CGGCCTGTCT GGGCCGCCCTC GTGGGGAGGG
661 AGGGGGCGCC CGGCCGCCCC GCGGCGACCC CGGGGCCTGG CCGCCACCAT GGGCTTCGAG
721 CTGGACCGCT TCGACGGCGA CGTGACCCG GACCTGAAGT GCGCGCTGTG CCACAAGGTC
781 CTGGAGGACC CGCTGACCAC GCCGTGCGGC CACGTCTTCT GCGCCGGCTG CGTGCTGCCC
841 TGGGTGGTGC AGGAGGGCAG CTGCCC GGCG CGCTGCCGCG GTCGCCTGTC GGCCAAAGAG
901 CTCAACCACG TCCTGCCGCT CAAGCGCCTT ATCCTCAAGC TGGACATCAA GTGCGCGTAC
961 GCGACGCGCG GCTGCGGCCG GGTGGTCAAG CTGCAGCAGC TGCCGGAGCA CCTCGAGCGC
1021 TGCGACTTCG CGCCCGCGCG CTGTCGCCAC GCGGGTTGCG GCCAGGTGCT GCTGCGGCGC
1081 GACGTGGAGG CGCACATGCG CGACGCGTGC GACGCGCGGC CAGTGGGCCG CTGCCAGGAG
1141 GGCTGCGGGC TACCCTTGAC GCACGGCGAG CAGCGCGCGG GCGGCCACTG CTGCGCGCGA
1201 GCGCTGCGGG CGCACAACGG CGCGCTCCAG GCCCGCCTGG GCGCGCTGCA CAAGGCGCTC
1261 AAGAAGGAGG CGCTGCGCGC TGGGAAGCGC GAGAAGTCGC TGGTGGCCCCA GCTGGCCGCG
1321 GCGCAGCTTG AGCTGCAGAT GACCGCGCTG CGCTACCAGA AGAAATTAC CGAATACAGC
1381 GCGCGCCTCG ACTCGCTCAG CCGCTGCGTG GCCGCGCCGC CCGGCGCAA GGGCGAAGAA
1441 ACCAAAAGTC TGACTCTTGT CCTGCATCGG GACTCCGGCT CCCTGGGATT CAATATTATT
1501 GGTGGCCGCG CGAGTGTGGA TAACCACGAT GGATCATCCA GTGAAGGAAT CTTTGTATCC
1561 AAGATAGTTG ACAGTGGGCC TGCAGCCAAG GAAGGAGGCC TGCAAATTCA TGACAGGATT
1621 ATTGAGGTCA ACGGCAGAGA CTTATCCAGA GCAACTCATG ACCAGGCTGT GGAAGCTTTC
1681 AAGACAGCCA AGGAGCCCAT AGTGGTGCAG GTGTTGAGAA GAACACCAAG GACCAAAATG
1741 TTCACGCCTC CATCAGAGTC TCAGCTGGTG GACACGGGAA CCCAAACCGA CATCACCTTT
1801 GAACATATCA TGGCCCTCAC TAAGATGTCC TCTCCCAGCC CACCCGTGCT GGATCCCTAT
1861 CTCTTGCCAG AGGAGCATCC CTCAGCCCAT GAATACTACG ATCCAAATGA CTACATTGGA
1921 GACATCCATC AGGAGATGGA CAGGGAGGAG CTGGAGCTGG AGGAAGTGGA CCTCTACAGA
1981 ATGAACAGCC AGGACAAGCT GGGCCTCACT GTGTGCTACC GGACGGACGA TGAAGACGAC

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Figure 3, continued

2041 ATTGGGATTT ATATCAGTGA GATTGACCCT AACAGCATTG CAGCCAAGGA TGGGCGCATC
 2101 CGAGAAGGAG ACCGCATTAT CCAGATTAAT GGGATAGAGG TGCAGAACCG TGAAGAGGCT
 2161 GTGGCTCTTC TAACCAGTGA AGAAAATAAA AACTTTTCAT TGCTGATTGC AAGGCCTGAA
 2221 CTCCAGCTGG ATGAGGGCTG GATGGATGAT GACAGGAACG ACTTTCTGGA TGACCTGCAC
 2281 ATGGACATGC TGGAGGAGCA GCACCACCAG GCCATGCAAT TCACAGCTAG CGTGCTGCAG
 2341 CAGAAGAAGC ACGACGAAGA CGGTGGGACC ACAGATACAG CCACCATCTT GTCCAACCAG
 2401 CACGAGAAGG ACAGCGGTGT GGGGCGGACC GACGAGAGCA CCCGTAATGA CGAGAGCTCG
 2461 GAGCAAGAGA ACAATGGCGA CGACGCCACC GCATCCTCCA ACCCGCTGGC GGGGCAGAGG
 2521 AAGCTCACCT GCAGCCAGGA CACCTTGGGC AGCGGCGACC TGCCCTTCAG CAACGAGTCT
 2581 TTCATTTTCGG CCGACTGCAC GGACGCCGAC TACCTGGGGA TCCCGGTGGA CGAGTGCGAG
 2641 CGCTTCCGCG AGCTCCTGGA GCTCAAGTGC CAGGTGAAGA GCGCCACCCC TTACGGCCTG
 2701 TACTACCCTA GCGGCCCCCT GGACGCCGCG AAGAGTGACC CTGAGAGCGT GGACAAGGAG
 2761 CTGGAGCTGC TGAACGAAGA GCTGCGCAGC ATCGAGCTGG AGTGCCTGAG CATCGTGCGC
 2821 GCCCACAAGA TGCAGCAGCT CAAGGAGCAG TACCGCGAGT CCTGGATGCT GCACAACAGC
 2881 GGCTTCCGCA ACTACAACAC CAGCATCGAC GTGCGCAGAC ACGAGCTCTC AGATATCACC
 2941 GAGCTCCCGG AGAAATCCGA CAAGGACAGC TCGAGCGCCT ACAACACAGG CGAGAGCTGC
 3001 CGCAGCACCC CGCTCACCTT GGAGATCTCC CCCGACAACCT CTTGAGGAG AGCGGCGGAG
 3061 GGCATCAGCT GCCCGAGCAG CGAAGGGGCT GTGGGGACCA CGGAAGCCTA CGGGCCAGCC
 3121 TCCAAGAATC TGCTCTCCAT CACGGAAGAT CCCGAAGTGG GCACCCCTAC CTATAGCCCG
 3181 TCCCTGAAGG AGCTGGACCC CAACCAGCCC CTGGAAAGCA AAGAGCGGAG AGCCAGCGAC
 3241 GGGAGCCGGA GCCCCACGCC CAGCCAGAAG CTGGGCAGCG CCTACCTGCC CTCCTATCAC
 3301 CACTCCCCAT ACAAGCACGC GCACATCCCG GCGCACGCCC AGCACTACCA GAGCTACATG
 3361 CAGCTGATCC AGCAGAAGTC GGCCGTGGAG TACGCGCAA GGCAGATGAG CCTGGTGAGC
 3421 ATGTGCAAGG ACCTGAGCTC TCCCACCCCG TCGGAGCCGC GCATGGAGTG GAAGGTGAAG
 3481 ATCCGCAGCG ACGGGACGCG CTACATCACC AAGAGGCCCG TCGGGGACCG CCTGCTGCGG
 3541 GAGCGCGCCC TGAAGATCCG GGAAGAGCGC AGCGGCATGA CCACCGACGA CGACGCGGTG
 3601 AGCGAGATGA AGATGGGGCG CTACTGGAGC AAGGAGGAGA GGAAGCAGCA CCTGGTGAAG
 3661 GCCAAGGAGC AGCGGCGGCG GCGCGAGTTC ATGATGCAGA GCAGGTTGGA TTGTCTCAAG
 3721 GAGCAGCAAG CAGCCGATGA CAGGAAGGAG ATGAACATTC TCGAACTGAG CCACAAAAG
 3781 ATGATGAAGA AGAGGAATAA GAAAATCTTC GATAACTGGA TGACGATCCA AGAACTCTTA
 3841 ACCCACGGCA CAAAATCCCC GGACGGCACT AGAGTATACA ATTCCTTCCT ATCGGTGACT
 3901 ACTGTATAAT TTTCACTTCT GCATTATGTA CATAAAGGAG ACCACTACCA CTGGGGTAGA
 3961 AATTCCTGCC TCGTTCAATG CGGCAAGTTT TTGTATATAA GATAAGTACG GTCTTCATGT
 4021 TTATAGTCCA AATTTGCAAA CCCTACAACCT CTGGGTGTCA TAGGTCTATT TTAAGGGAAG

Figure 3, continued

4081 AGAGAGAAAA ACACCCTTAC TATCTTGGAA GGCAATATTA ACAAACAGAG CTTTTTTCAA
4141 ATAGCAATTG TACTTTTCTA CCTGTACCCT TTTACATAAA GTGTTTAAAT TTCAGAAAGA
4201 TCTTTTATTA AGCATACTTT CACAGAATAA CTTGTTTAAA CTATATTCAT ATAAAAAAGT
4261 TAAACACGCT TTTTTTCCTG CCTAAAACAC AAATACAACCT GCCAGTATGT ATTTTAAATG
4321 GAACCCTATT TTATAATGGT ACGTTACTGA ATGTGTTTCA TATGCGTGAC CGTTAAGATA
4381 TTATCATTTA GGTGAAGGTT TCAACTCAAA ACCACCCAAC CCGGTGGTTA ACGATTTAAT
4441 ACATATAACC AAACCGGCAG CGTTTAGAGT TGGGATATAC ATTTAAACAT TTCCTGGTT
4501 AAGGTTCCCA AGAGAGTGTA AAGGTTTTAG CAGAAAGCAA AATATCTTGC ATCTTTATGG
4561 AAGTTTAAAG CATGTTTGCA AATATTGCAG CCCATTGAAA GAATTTGCAT GTACAGGAAA
4621 GTTGTGGATG GAGACGGTTT GTGGAATTTT AAGTGCTCAT TGTAAGTAAAC TTTTGCTTTG
4681 TAGATTTGAA GGTACAGACT TATACAGGCA AGTTCACAAA ATCATGATTA GTTACAAACA
4741 GTAAAATGAA GTTAAAATAA ATTATTATTT TCT

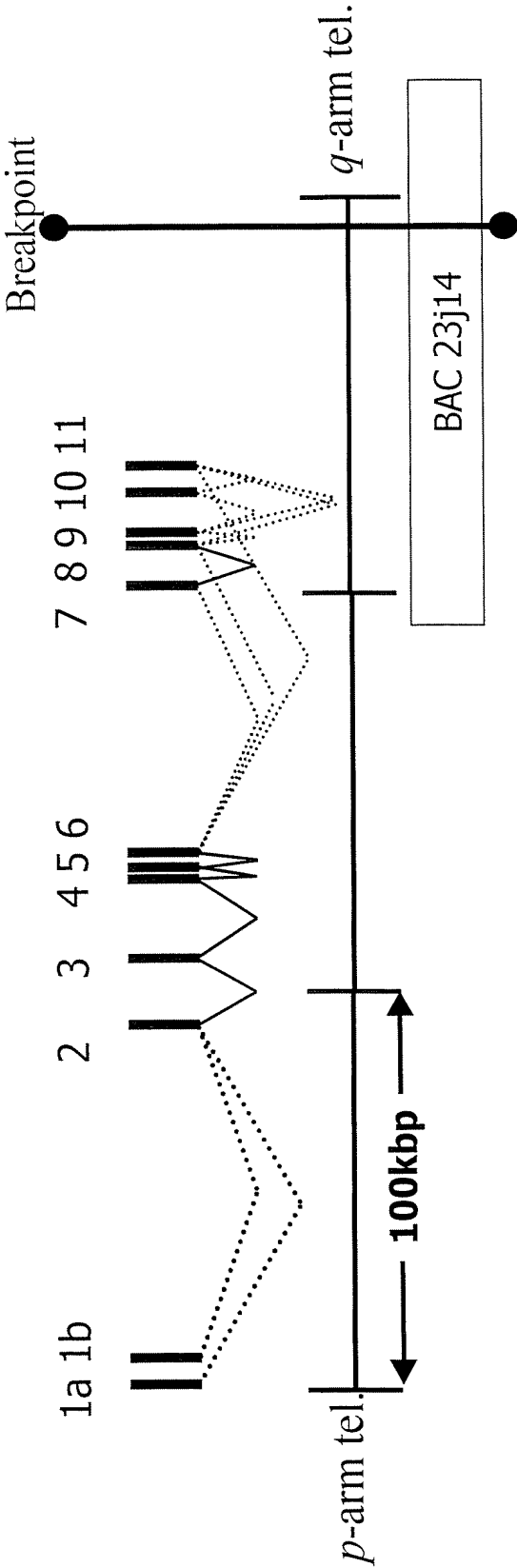
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Figure 4 (SEQ ID NO: 2)

1 MGFELDRFDG DVD~~PDLK~~CAL ~~CHKVLED~~PLT TPCGHVFCAG CVLPWVVQEG ~~SCPARCR~~GRL
61 SAKELNHVLP LKRLILKLDI KCAYATRGCG RVVKLQQLPE ~~HLERCD~~FAPA RCRHAGCGQV
121 ~~LLRRD~~VEAHM RDACDARPVG RCQEGCGLPL THGEQ~~RAGGH~~ CCARALRAHN GALQARLGAL
181 HKALKKEALR AGKREKSLVA QLAA~~AQLE~~LQ MTALRYQKKF TEYSARLDSL SRCVAAPPGG
241 KGEET~~KSL~~TL VLHRDSGSLG FNIIGGRPSV DNHDGSSSEG IFVSKI~~VDSG~~ PAAKEGGLOI
301 ~~HDRIIE~~VNGR DLSRATHDQA VEA~~FKT~~AKEP IVVQVLR RTP RTKMFTPPSE SQLVDTGTQT
361 DITFEHIMAL TKMSSPSPPV LDPYLLPEEH PSAHEYYDPN DYIGDIHQEM DREELELEE~~V~~
421 ~~DLYRM~~NSQDK LGLTVCYRTD DEDDIGIYIS EIDPNSIAAK DGRIREGDRI IQINGIEVQ~~N~~
481 ~~REEA~~VALLTS EENKNFSLLI ARPELQ~~LDEG~~ WMDDDRND~~FL~~ DDLHMDMLEE QHHQAMQFTA
541 SVLQQKKHDE DGGTTDTATI LSNQHEKDSG VGR~~TDEST~~RN DESSEQENNG DDATA~~SSN~~NPL
601 AGQRKL~~TCS~~Q DTLGSGDLPF SNESFISADC TDADYLGIPV DECERFRELL ELKCQVKSAT
661 PYGLYYPSGP LDAGKSDPES VDKELELLNE ELRSIELECL SIVRAHKMQQ LKEQYRESWM
721 LHNSGFRNYN TSIDVRRHEL SDITELPEKS DKDSS~~SAYNT~~ GESCRSTPLT LEISPDNSLR
781 RAAEGISCPS SEGAVGTTEA YGPASKNLLS ITEDPEVGTP TYSPSLKELD PNQPLESKER
841 RASDGSRSPT PSQKLGSAYL PSYHHSPYKH AHIPAH~~AQHY~~ QSYMQLIQQK SAVEYAQSQM
901 SLVSMCKDLS SPTPSEPRME WKVKIRSDGT RYITKRPVRD RLLRERALKI REERSGMTTD
961 DDAVSEM~~KMG~~ RYWSKEERKQ HLVKAKEQRR RREFMMQSRL DCLKEQQAAD DRKEMNILEL
1021 SHKKMMKKRN KKIFDNWMTI QELLTHG~~TKS~~ PDGTRVYNSF LSVTTV

Figure 5



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Figure 6

1a (SEQ ID NO: 3)

atcttcctcctgctctggctgtgtgaagatctgcctccttcctcttcggcttcatgcatgat
cgtaagtttcctgaggcctcctcagccatgcttcctgcatagcctgcagaaat

1b (SEQ ID NO: 4)

cccggtccctcgcaaagccgctgccatcccggagggcccagccagcgggctcccggaggct
ggccgggcaggcgtggtgcgcggtaggagctgggcgcgcacggctaccgcgcgtggaggaga
cactgccctgccgcgatggggggccggggcgctccttcacgccgtaggcaagcggggcgcg
gctgcggtacctgccaccgggagctttcccttccttctcctgctgctgctgctctgcaccc
agctcgggggaggacagaagaaaaaggag

2-6 (SEQ ID NO: 5)

These exons have been joined together as they are always
spliced in this way.

aatcttttagctgaaaaagtagagcagctgatggaatggagttccagacgctcaatcttcg
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7 (SEQ ID NO: 6)

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ga

8 (SEQ ID NO: 7)

atgccgctatcaccatggggatgggttcttctaaatgaagcagcaacttcgaaaggcgatgtt
ggaaaaagacgga

8+ (SEQ ID NO: 8)

This is identical to 8 except a cryptic splice acceptor
upstream is employed.

Tttaaccattctggaacattgtgttcagagccagaaaaattaatagattttattcacatcta
tgtctacggcttccttgacaactactgcagatgccgctatcaccatggggatgggttcttcta
aatgaagcagcaacttcgaaaggcgatgttggaaaaagacgga

Figure 6, continued

9 (SEQ ID NO: 9)

taatttgccctagtgaggattgggcctgggtggtcttcttcttcagttttctactttcaatattt
cgttccaagtaccacggctatccttatag

10 (SEQ ID NO: 10)

tgatctggactttgagtgagaagatgtgatttggaccatggcacttaaaaactctataacct
cag

11 (SEQ ID NO: 11)

ctttttaattaaatgaagccaagtgggatttgcataaagtgaatgtttaccatgaagataaa
ctgttcctgactttataactattttgaattc

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Figure 7

Alternative start exons

1a: (SEQ ID NO: 12)

MEWSSRRSIFRMNGDKFRKFIKAPPRNYS..... (encoded by exon 2).

1b: (SEQ ID NO: 13)

MGARGAPSRRRQAGRRLRYLPTGSFPFLLLLLLLLLCIQLGGGQKKKENLLAEKVEQLMEWSSR
RSIFRMNGDKFRKFIKAPPRNYS.....

Transcript options

2-6,7,8,9,10,11 (SEQ ID NO: 14/15)
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gcacttaaaaactctataacctcagctttttaattaaatgaagccaagtgggatttgcataa
agtgaatgtttaccatgaagataaactgttcctgactttataactattttgaattc

(MGARGAPSRRRQAGRRLRYLPTGSFPFLLLLLLLLLCIQLGGGQKKKENLLAEKVEQL) MEWS
SRRSIFRMNGDKFRKFIKAPPRNYSMIVMFTALQPQRQCSVCRQANEYQILANSWRYSSAF
CNKLFFSMVDYDEGTDVDFQQLNMNSAPTFMHFPPKGRPKRADTFDLQRIGFAAEQLAKWIAD
RTDVHIRVFRPPNYSGTIALALLVSLVGGLLYLRRNNLEFIYNKTGWAMVSLCIVFAMTSGQ
MWNHIRGPPYAHKNPHNGQVSYIHGSSQAQFVAESHIILVLNAAITMGMVLLNEAATSKGDV
GKRRIICLVGLGLVVFSSFLLSIFRSKYHGYPSDLDFE

Figure 7, continued

2-6,7,8,9,11 (SEQ ID NO: 16/17)

aatcttttagctgaaaaagtagagcagctgatggaatggagttccagacgctcaatcttccg
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agtaccacggctatccttatagcttttttaattaaatgaagccaagtgggatttgcataaagt
gaatgtttaccatgaagataaactgttcttgactttataactattttgaattc

(MGARGAPSRRRQAGRRLRYLPTGSFPFLLLLLLLLCIQLGGGQKKKENLLAEKVEQL) MEWS
SRRSIFRMNGDKFRKFIKAPPRNYSMIVMFTALQPQRQCSVCRQANEEYQILANSWRYSSAF
CNKLFFSMVDYDEGTDV FQQLNMNSAPT FMHFPPKGRPKRADTFDLQORIGFAAEQLAKWIAD
RTDVHIRVFRPPNYSGTIALALLVSLVGGLLYLRRNNLEFIYNKTGWAMVSLCIVFAMTSGQ
MWNHIRGPPYAHKNPHNGQVSYIHGSSQAQFVAESHIILVLNAAITMGMVLLNEAATSKGDV
GKRRIICLVGLGLVFFFSFLLSIFRSKYHGYPSFLIK

2-6,11 (SEQ ID NO: 18/19)

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ttgaattc

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Figure 7, continued

(MGARGAPSRRRQAGRRLRYLPTGSFPFLLLLLLLLLCIQLGQGQKKKENLLAEKVEQL) MEWS
SRRSIFRMNGDKFRKFIKAPPRNYSMIVMFTALQPQRQCSVCRQANEYYQILANSWRYSSAF
CNKLFFSMVDYDEGTDVFQQLNMNSAPTFMHFPPKGRPKRADTFDLQRIGFAAEQLAKWIAD
RTDVHIRVFRPPNYSGTIALALLVSLVGGLLYLRRNNLEFIYNKTGWAMVSLCIVFAMTSGQ
MWNHIRGPPYAHKNPHNGQVLFN

2-6,7,8,11 (SEQ ID NO: 20/21)

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(MGARGAPSRRRQAGRRLRYLPTGSFPFLLLLLLLLLCIQLGQGQKKKENLLAEKVEQL) MEWS
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CNKLFFSMVDYDEGTDVFQQLNMNSAPTFMHFPPKGRPKRADTFDLQRIGFAAEQLAKWIAD
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GKRRTF

2-6,8+,9,11 (SEQ ID NO: 22/23)

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ggttttcagaccaccaactactctggtaccattgctttggccctgttagtgctcgcttggtg
gaggtttgctttatttgagaaggaacaacttggagttcatctataacaagactgggtgggccc
atgggtgtctctgtgtatagtctttgctatgacttctggccagatgtggaaccatatccgtgg
acctccatatgctcataagaacccacacaatggacaagtgtttaaccattctggaacattgt
gttcagagccagaaaaattaatagat

Figure 7, continued

tttattcacatctatgtctacggcttccttgacaactactgcagatgccgctatcaccatgg
ggatgggttcttctaaatgaagcagcaacttcgaaaggcgatggttgaaaaagacggataatt
tgcctagtgggattgggcctgggtggtcttcttcttcagttttctactttcaatatttcgcttc
caagtaccacggctatccttatagcttttttaattaaatgaagccaagtgggatttgcataaa
gtgaatgtttaccatgaagataaactgttcctgactttataactattttgaattc

(MGARGAPSRRRQAGRRLRYLPTGSFPFLLLLLLLLLCIQLGGGQKKKENLLAEKVEQL) MEWS
SRRSIFRMNGDKFRKFIKAPPRNYSMIVMFTALQPQRQCSVCRQANEYYQILANSWRYSSAF
CNKLFFSMVDYDEGTDVFQQLNMNSAPTFMHFPPKGRPKRADTFDLQRI GFAAEQLAKWIAD
RTDVHIRVFRPPNYSGTIALALLVSLVGGLLYLRRNNLEFIYNKTGWAMVSLCIVFAMTSGQ
MWNHIRGPPYAHKNPHNGQVFNHSGTLCSEPEKLIDFIHIYVYGFLDNYCRCRYHHGDGSSK

2-6,8+,11 (SEQ ID NO: 24/25)

aatcttttagctgaaaaagtagagcagctgatggaatggagttccagacgctcaatcttccg
aatgaatggtgataaattccgaaaatttataaaggcaccacctcgaaactattccatgattg
ttatgttcaactgctcttcagcctcagcggcagtggttctgtgtgcaggcaagctaataagaa
tatcaaatactggcgaactcctggcgctattcatctgctttttgtaacaagctcttcttcag
tatgggtggactatgatgaggggacagacgtttttcagcagctcaacatgaactctgctccta
cattcatgcattttcctccaaaaggcagacctaagagagctgatacttttgacctccaaaga
attggatttgagctgagcaactagcaaatggattgctgacagaacggatggttcatatctcg
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gaggtttgctttatttgagaaggaacaacttgagttcatctataacaagactgggtgggccc
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acctccatatgctcataagaacccacacaatggacaagtgtttaaccattctggaacattgt
gttcagagccagaaaaattaatagattttattcacatctatgtctacggcttccttgacaac
tactgcagatgccgctatcaccatggggatggttcttctaaatgaagcagcaacttcgaaag
gcgatggttgaaaaagacggacttttttaattaaatgaagccaagtgggatttgcataaagtg
aatgtttaccatgaagataaactgttcctgactttataactattttgaattc

(MGARGAPSRRRQAGRRLRYLPTGSFPFLLLLLLLLLCIQLGGGQKKKENLLAEKVEQL) MEWS
SRRSIFRMNGDKFRKFIKAPPRNYSMIVMFTALQPQRQCSVCRQANEYYQILANSWRYSSAF
CNKLFFSMVDYDEGTDVFQQLNMNSAPTFMHFPPKGRPKRADTFDLQRI GFAAEQLAKWIAD
RTDVHIRVFRPPNYSGTIALALLVSLVGGLLYLRRNNLEFIYNKTGWAMVSLCIVFAMTSGQ
MWNHIRGPPYAHKNPHNGQVFNHSGTLCSEPEKLIDFIHIYVYGFLDNYCRCRYHHGDGSSK

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Figure 8

IAG2_HUMAN	MAAR-----WRFWCVSVTMVVALIVCDVPSASA
N33_HUMAN	MGARGAPSRRRQAGRRLRYLPTGSFPFLLLLLLLLCIQLGGG
DROS._CG7830	-----MRL LHKTLLSGLLVVALFAIYAAQ
Celegans_g304348	-----MLLAVYESAQ
Yeast_Ost3p	-----MNWLFLVSLVFFCGV
Yeast_Ost6p	-----MKWCSTYII IWLAIIFHKF

IAG2_HUMAN	QRKKE-MVLSEKVSQLMWETNKRVPVIRMNGDKFRRLVKAPP
N33_HUMAN	QKKKE-NLLAEKVEQLMEWSSRRSIFRMNGDKFRKF I KAPP
DROS._CG7830	SKSKTGLSLSEKVQNLVDMNAKKPLLRFNGPKFREYVKSAP
Celegans_g304348	QQT-----LEDKVQNLVDLTSRQSIVKFNMDKWKTIVRMQP
Yeast_Ost3p	STHPALAMSSNRLKLANKSPKK---I I PLKDSSFENILAP
Yeast_Ost6p	QKSTA--TASHNIDDILQLKDDTGVITVTADNYPLLSRGVP

IAG2_HUMAN	--RNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSS
N33_HUMAN	--RNYSMIVMFTALQPQRQCSVCRQANEYQILANSWRYSS
DROS._CG7830	--RNYSMIVMLTALAPSRQCQICRHAHDEF AIVANSYRFSS
Celegans_g304348	--RNYSMIVMFTALSPGVQCPICKPAYDEFMIVANSHRYTS
Yeast_Ost3p	PHENAYIVALFTATAPEIGCSLCLELESEYDTIVASWFDDH
Yeast_Ost6p	GYFNILYITMRGTNSNGMSCQLCHDFEKTYHAVADVIRSQA CYST.

IAG2_HUMAN	AFTN-----RIFFAMVDFDEG---SDVFQMLNMNSAPTF
N33_HUMAN	AFCN-----KLFFSMVDYDEG---TDVFQQLNMNSAPTF
DROS._CG7830	TYSN-----KLFFAMVDFDDG---SEVFQLLRLNTAPVF
Celegans_g304348	SEGDRR---KVFFGIVDYEDA---PQIFQOMNLNTAPIL
Yeast_Ost3p	PDAKSSNSDTSIFFTKVNLEDPSKTIPKAFQFFQLNNVPRL
Yeast_Ost6p	PQSLN-----LFFTVDVNEV---PQLVKDLKLQNVPHL

IAG2_HUMAN	INFPAK-GKPKRGDTYELQVRG--FSAEQIARWIADR----
N33_HUMAN	MHFPPK-GRPKRADTFDLQRIG--FAAEQLAKWIADR----
DROS._CG7830	MHFPAK-GKPKGADTMDIHRVG--FAADSI AKFVAER----
Celegans_g304348	YHFGPKLGAKKRPEQMD FQRQG--FDADAIGRFVADQ----
Yeast_Ost3p	FIEKPNSPSILDHSVISISTDTGSERMKQIIQAIKQF----
Yeast_Ost6p	VVYP PAESNKQSQFEWKTS PFYQYSLVPENAENTLQFGDFL

IAG2_HUMAN	-TDVNIRVIRPPNYAGPLMLGLLLAVIGGLVYLRRSNMEF-
N33_HUMAN	-TDVHIRVFRPPNYS GTIALALLVSLVGGLLYLRRNNLEF-
DROS._CG7830	-TDITIRIFRPPNYS GTVAMITLVALVGSFLYIRRNLEF-
Celegans_g304348	-TEVHVRVIRPPNYTAPVVIALFVALLGLMYMKRNSLDF-
Yeast_Ost3p	-SQVNDFSLHLPMDWTP IITSTIITFITVLLFKKQSKLMFS
Yeast_Ost6p	AKILNISITVPQAFNVQEFVYFVACMVVFIFIKKVILPKV

*****TM 1*****cccccccccc

SEQ ID NO: 26 IAG2_HUMAN; SEQ ID NO: 27 N33_HUMAN; SEQ ID NO: 28 N33_HUMAN;
 SEQ ID NO: 29 N33_HUMAN; SEQ ID NO: 30 DROS._CG7830; SEQ ID NO: 31
 Celegans_g304348; SEQ ID NO: 32 Yeast_Ost3p; SEQ ID NO: 33 Yeast_Ost6p

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Figure 8, continued

IAG2_HUMAN	-LFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKNPHTG
N33_HUMAN	-IYNKTGWAMVSLCIVFAMTSGQMWNHIRGPPYAHKNPHNG
DROS._CG7830	-LYNKNLWGAIIVFFCFAMISGQMWNHIRGPPPLVHKS-QNG
Celegans_g304348	-LFNRTVWGFVCLAITFIFMSGQMWNHIRGPPFMITNPNTK
Yeast_Ost3p	IISRIIWATLSTFFIICMISAYMFNQIRNTQLAGVGPKE
Yeast_Ost6p	TNKWKLFSMILSLGILLPSITGYKFVEMNAIPFIARDAKN-
	CCCCC*****TM 2*****

IAG2_HUMAN	HVNYIHGSSQAQFVAETHIVLLFNNGVTLGMVLLCEAATSD
N33_HUMAN	QVSYIHGSSQAQFVAESHIILVLNAAITMGMVLLNEAATSK
DROS._CG7830	GVAYIHGSSQGQLVETIYIVMFLNAMIVLGMILLIESGTPK
Celegans_g304348	EPSFIHGSTQFQLIAETIYIVGLLYALIAIGFICVNEAADQS
Yeast_Ost3p	VMYFLPNEFQHQFAIETQVMVLIYGTLAALVVVLVKGIQFL
Yeast_Ost6p	RIMYFSGGSGWQFGIEIFSVSLMYIVMSALSULLIYVPKIS
	*****TM 3*****CCCCCCCC

IAG2_HUMAN	MDIGKR-----KIMCVAGIGLVVLFWSML
N33_HUMAN	GDVGKR-----RIICLVGLGLVVFFFSFLL
DROS._CG7830	AHN-KN-----RIMAMTGLVLLTVFFFSFLL
Celegans_g304348	NSKDRKNAGKKLNPLSLNIPTNTLAIAGLVCICVFFFSFLL
Yeast_Ost3p	RSHLYP-----ETKKAYFIDAILASFALFIYVFFAALT
Yeast_Ost6p	CVSEKMR-----GLLSSFLACVLFFYSYFI
	CCCCCCCCCCCCCCCCCCCC*****TM 4*****
	TF (3)

IAG2_HUMAN	SIFRSKYHGYPSFLMS-----
N33_HUMAN	SIFRSKYHGYPSDLDFE- (1) -----
DROS._CG7830	SVFRSKAQGYPIVSCSNRIDCSPVPVQVHPISFL
Celegans_g304348	SVFRSKYRGYPYSFLFA-----
Yeast_Ost3p	TVFTIKSPAYPFLLRLSAPFK-----
Yeast_Ost6p	SCYLIKPNPGYPIVF-----

FLIK (2)

SEQ ID NO: 26	IAG2_HUMAN
SEQ ID NO: 27	N33 1_HUMAN
SEQ ID NO: 28	N33 2_HUMAN
SEQ ID NO: 29	N33 3_HUMAN
SEQ ID NO: 30	DROS._CG7830
SEQ ID NO: 31	Celegans_g304348
SEQ ID NO: 32	Yeast_Ost3p
SEQ ID NO: 33	Yeast_Ost6p

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Figure 9

C-termini of N33 splice forms

N33_67811_Translated_-_Longe	LVSLVGGLLYLRRNNLEFIYNKTGWAMVSLCIVFAMTSGQMWNHIRGPPY
N33_67891011_Translated_-_Lo	LVSLVGGLLYLRRNNLEFIYNKTGWAMVSLCIVFAMTSGQMWNHIRGPPY
N33_678911_Translated_-_Long	LVSLVGGLLYLRRNNLEFIYNKTGWAMVSLCIVFAMTSGQMWNHIRGPPY
N33_611_Translated_-_Longest	LVSLVGGLLYLRRNNLEFIYNKTGWAMVSLCIVFAMTSGQMWNHIRGPPY
N33_68+911_Translated_-_Long	LVSLVGGLLYLRRNNLEFIYNKTGWAMVSLCIVFAMTSGQMWNHIRGPPY
N33_68+11_Translated_-_Longe	LVSLVGGLLYLRRNNLEFIYNKTGWAMVSLCIVFAMTSGQMWNHIRGPPY

N33_67811_Translated_-_Longe	AHKNPHNGQVSYIHGSSQAQFVAESHIILVLNAAITMGMVLLNEAATSKG
N33_67891011_Translated_-_Lo	AHKNPHNGQVSYIHGSSQAQFVAESHIILVLNAAITMGMVLLNEAATSKG
N33_678911_Translated_-_Long	AHKNPHNGQVSYIHGSSQAQFVAESHIILVLNAAITMGMVLLNEAATSKG
N33_611_Translated_-_Longest	AHKNPHNGQVLEFN-----
N33_68+911_Translated_-_Long	AHKNPHNGQVFNHSG----TLCSEPEKLIDFIHIYVYG--FLDNYCRCRY
N33_68+11_Translated_-_Longe	AHKNPHNGQVFNHSG---TLCSEPEKLIDFIHIYVYG--FLDNYCRCRY

N33_67811_Translated_-_Longe	DVGKRRTE-----
N33_67891011_Translated_-_Lo	DVGKRRICLVGLGLVVFFFSFLLSIFRSKYHGYPYSDDLDFE
N33_678911_Translated_-_Long	DVGKRRICLVGLGLVVFFFSFLLSIFRSKYHGYPYSFLIK-
N33_611_Translated_-_Longest	-----
N33_68+911_Translated_-_Long	HHGDGSSK-----
N33_68+11_Translated_-_Longe	HHGDGSSK-----

N33_67811_Translated_-_Longe	(SEQ ID NO: 34)
N33_67891011_Translated_-_Lo	(SEQ ID NO: 35)
N33_678911_Translated_-_Long	(SEQ ID NO: 36)
N33_611_Translated_-_Longest	(SEQ ID NO: 37)
N33_68+911_Translated_-_Long	(SEQ ID NO: 38)
N33_68+11_Translated_-_Longe	(SEQ ID NO: 39)

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Figure 10 (SEQ ID NO: 40)

Published GRIK4 nucleic acid sequence (accession NM_014619).

```
1 atgccccgcg tctcggcgcc tttggtgctg cttcctgcgt ggctcgtgat ggtcgcctgc
61 agccccgact ccttgaggat cgctgctatc ttggacgacc ccatggagtg cagcagaggg
121 gagcggctct ccatcaccct ggccaagaac cgcatacaacc gcgctcctga gaggctgggc
181 aaggccaagg tcgaagtgga catcttttag cttctcagag acagcgagta cgagactgca
241 gaaacctatgt gtcagatcct ccccaagggg gtggtcgtcg tcctcggacc atcgtccagc
301 ccagcctcca gctccatcat cagcaacatc tgtggagaga aggaggtccc tcacttcaaa
361 gtggccccag aggagttcgt caagttccag ttccagagat tcacaaccct gaacctccac
421 cccagcaaca ctgacatcag cgtggctgta gctgggatcc tgaacttctt caactgcacc
481 accgcctgcc tcatctgtgc caaagcagaa tgccttttaa acctagagaa gctgctccgg
541 caattcctta tctccaagga cacgctgtcc gtccgcatgc tggatgacac ccgggacccc
601 accccgctcc tcaaggagat ccgggacgac aagaccgcca ccatcatcat ccacgccaac
661 gcctccatgt cccacaccat cctcctgaag gcagccgaac ttgggatggt gtcagcctat
721 tacacataca tcttactaa tctggagttc tcaactcaga gaacggacag ccttgtggat
781 gatcgtgtca acatcctggg attttccatt ttcaaccaat cccatgcttt cttccaagag
841 tttgccaga gcctcaacca gtccctggcag gagaactgtg accatgtgcc cttactggg
901 cctgcgctct cctcggccct gctgtttgat gctgtctatg ctgtggtgac tgcggtgcag
961 gaactgaacc ggagccaaga gatcggcgtg aagcccttgt cctgcggctc ggcccagatc
1021 tggcagcacg gcaccagcct catgaactac ctgcgcatgg tagaattgga aggtcttacc
1081 ggccacattg aattcaacag caaaggccag aggtccaact acgctttgaa aatcttacag
1141 ttcacaagga atggttttcg gcagatcggc cagtggcacg tggcagaggg cctcagcatg
1201 gacagccacc tctatgcctc caacatctcg gacactctct tcaacaccac cctggtcgtc
1261 accaccatcc tggaaaaccc atatttaatg ctgaagggga accaccagga gatggaaggc
1321 aatgaccgct acgagggctt ctgtgtggac atgctcaagg agctggcaga gatcctccga
1381 ttcaactaca agatccgcct gggtggggat ggcggtgtac gcgttcccga ggccaacggc
1441 acctggacgg gaatggtcgg ggagctgacg gctaggaaaag cagatctggc tgtggcaggc
1501 ctcaccatta cagctgaacg ggagaagggtg attgatttct ctaagccatt catgactctg
1561 ggaattagca ttctttaccg cattcatatg ggacgcaaac ccggtatatt ctccttcctg
1621 gacccatttt ctccgggcgt ctggctcttc atgcttctag cctatctggc cgtcagctgt
1681 gtccctcttc tggtggctcg gttgacgcc tacgagtggg acagcccaca ccatgtgccc
1741 cagggccggg gcaacctcct ggtgaaccag tactccctgg gcaacagcct ctggtttccg
1801 gtcggggggg tcatgcagca gggctccacc atcgccctc gcgccttatc caccgctgt
1861 gtcagtggcg tctggtgggc attcacgctg atcatcatct catcctacac ggccaacctg
1921 gcagccttcc tgaccgtgca gcgcatggat gtgccatttg agtcagtgga tgacctggct
1981 gaccagaccg ccattgaata tggcacaatt cacggagggt ccagcatgac cttcttccaa
2041 aattcccgct accagaccta ccaacgcatt tgggaattaca tgtattccaa gcagcccagc
2101 gtgttcgtga agagcacaga ggaggggaat gccaggggtg tgaattccaa ctacgccttc
2161 ctctggaat ccaccatgaa cgagtactat cggcagcgaa actgcaacct cactcagatt
2221 gggggcctgc tggacaccaa gggctatggg attggcatgc cagtcggctc ggttttccgg
2281 gacgagtttg atctggccat tctccagctg caggagaaca accgcctgga gatcctgaag
2341 cgcaaattgg ggaaggagg gaagtgcctc aaggagggaag atcacagagc taaaggcctg
2401 ggaatggaga atattgggtg aatctttgtg gttcttattt gtggcttaat cgtggccatt
2461 tttatggcta tgttgagttt tttatggact ctcagacact cagaagcaac tgaggtgtcc
2521 gtctgccagg agatggtgac cgagctgcgc agcattatcc tgtgtcagga cagtatccac
2581 cccgcgccgc ggcgcgccgc agtccgcgcg ccccgcccc ccacccccga ggagcgccga
2641 ccgcggggca cggcgacgct cagcaacggg aagctgtgcg gggcagggga gcccgaccag
2701 ctgcgcgaga gactggcgca ggaggccgcc ctggtggccc gcggtgcac gcacatccgc
2761 gtctgccccg agtgccgcgc cttccagggc ctgcgggcac ggccgtcgcc cgccgcagc
2821 gaggagagcc tggagtggga gaaaaccacc aacagcagcg agcccagata g
```

Figure 11 (SEQ ID NO: 41)

Published GRIK4 protein sequence (accession NP_055434).

MPRVSAPLVLLPAWLVMVACSPHSLRIAAILDDPMECSRGERLSITLAKNRINRAPERLGKA
KVEVDIFELLRDSEYETAETMCQILPKGVAVLGPSSSPASSSIISNICGEKEVPHFKVAPE
EFVKFQFQRFTTNLNLHPSNTDISVAVAGILNFFNCTTACLICAKAECLLNLEKLLRQFLISK
DTLSVRMLDDTRDPTPLLKEIRD DKTATIIHANASMSHTILLKAAELGMVSAYYTYIFTNL
EFSLQRTDSLVD DRVNILGFSIFNQSHAFFQEFAQSLNQSWQENCDHVPFTGPALSSALLFD
AVYAVVTAVQELNRSQEIGVKPLSCGSAQIWQHGTSLMNYLRMVELEGLTGHI EFNSKGQRS
NYALKILQFTRNGFRQIGQWHVAEGLSMDSHLYASNISDTLFNTTLVVTITILENPYLMLKGN
HQEMEGND RYEGFCVDMLKELAEILRFNYKIRLVGDGVYGVPEANGTWTGMVGELIARKADL
AVAGLTITAEREKVIDFSKPFMTLGISILYRIHMGRKPGYFSFLDPFSPGVWLFMLLAYLAV
SCVLFLVARLTPYEWYSPHPCAQGRCNLLVNQYSLGNSLWFPVGGFMQOGSTIAPRALSTRC
VSGVWVAFTLIIISSYTANLAAFLT VQRM DVP IESVDDLADQTAIEYGTIHGGSSMTFFQNS
RYQTYQRMWNMYMYSKQPSV FVKSTEEGIARVLNSNYAFLLESTMNEYRQRNCNLTOIGLL
DTKGYGIGMPVGSVFRDEFDLAILQLQENNRLEILKRKWWEGGKCPKEEDHRAKGLGMENIG
GIFVVLICGLIVAI FMAMLEFLWTLRHSEATEVSVCQEMVTELRSIILCQDSIHPRRRRAAV
PPRPPIPEERRPRGTATLSNGKLCGAGEPDQLAQRLAQEAALVARGCTHIRVCPECRRFQG
LRARSPARSEESLEWEKTTNSSEPE

Figure 12

Cytogenetic Position	Description	Breakpoint YAC Clones	Breakpoint BAC Clones (Acc. No.)
2p12	Inversion breakpoint	915_f_7	-
2q32.1	Inversion breakpoint	941_h_12	RP11-358M9 (AC020595)
2q21.3	Translocation breakpoint	766_c_12	RP11-250H22 (AC011996)
11q23.3	Upper insertion breakpoint	936_d_9	RP11-89P5 (AC009641)
11q24.2	Translocation/Insertion breakpoint	749_d_2	RP11-687M24 (AP001007)

Figure 13

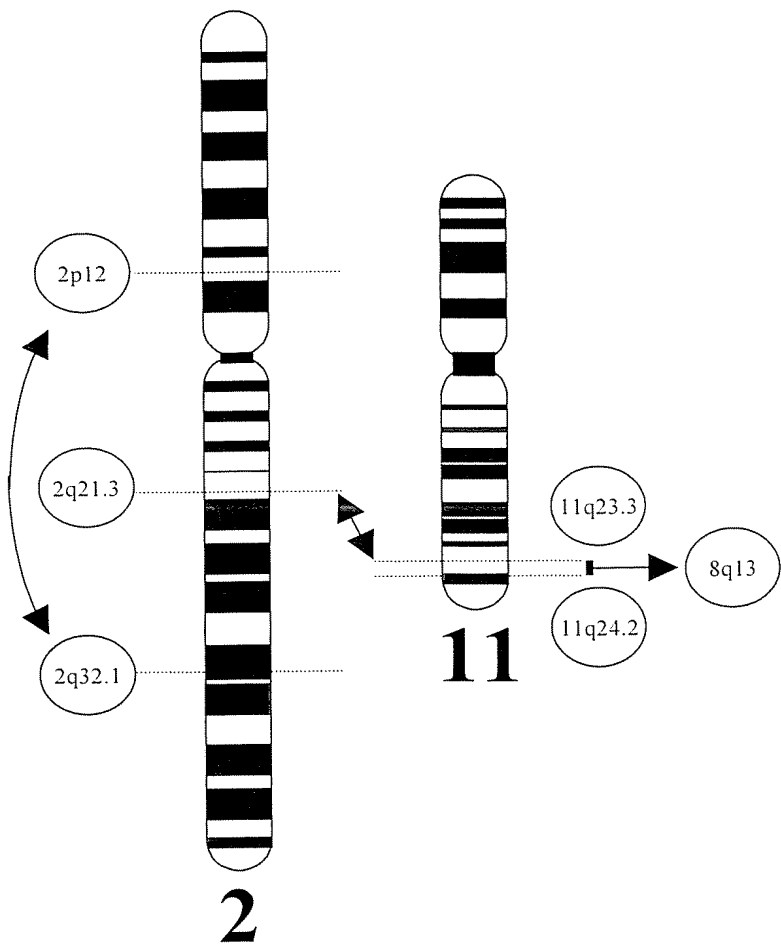
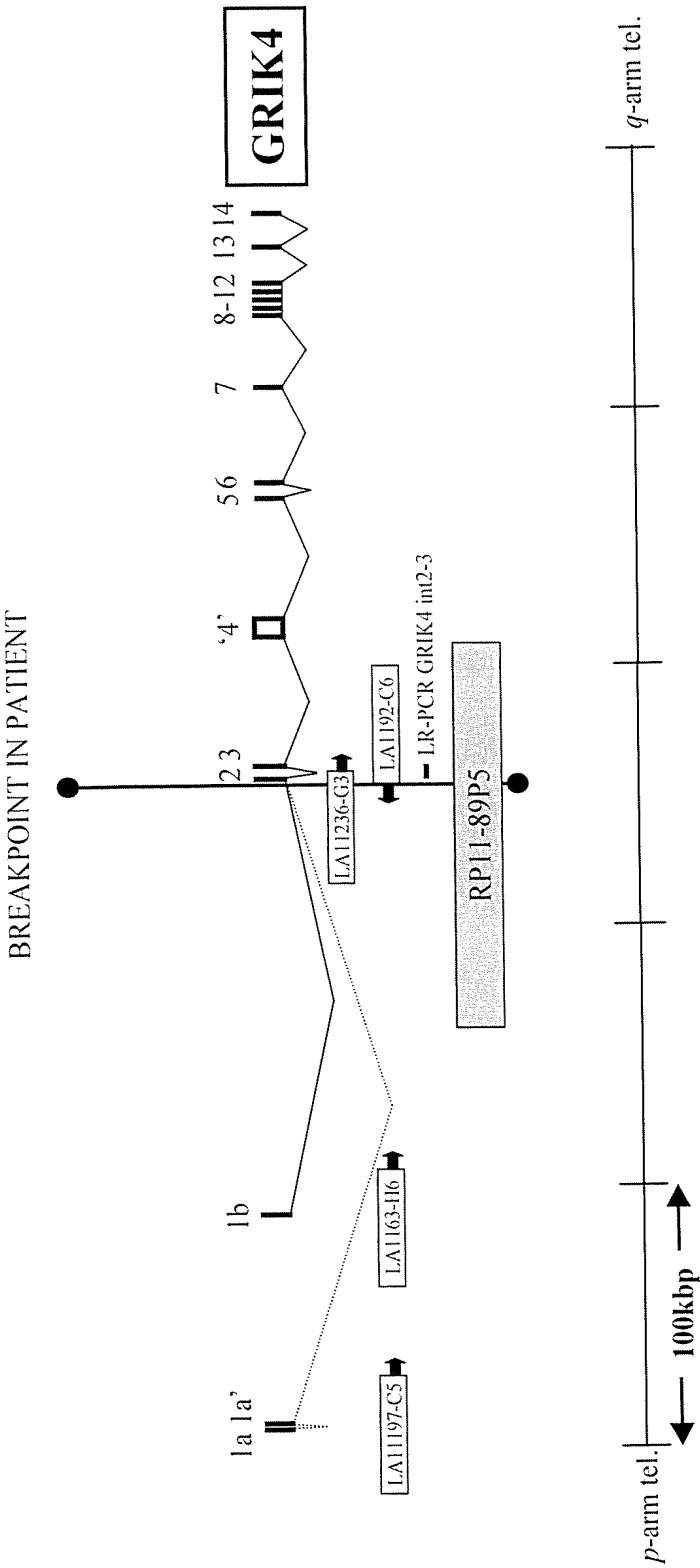


Figure 14



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Figure 15

Exon 1a (SEQ ID NO: 42)

GCGTGGTAGCATGTGCCTGTAATCCCAGTGCTTTGGGACACCGAGGCAGGAGGATCACT
CGAGCCCAGGAGTGCGAGGCTGCAgtgagttatgatcatac

Exon 1a' (SEQ ID NO: 43/44)

agatttgtccttctctgccagGTGACGCTAGACTTCAGGAAGACCCCCCATTTCTGCTCCACT
CCTGGGCTTGGAGAAGAGTACAGCTGCTCTTGACTGGTGGGACCTTTTGCTGGCTAGGGGTG
ATGGGAGAAGCAAGAGAGGGATCCACACACCTGCGCTTAGCTTTCTATGACCTGGGCGGATG
GAGGCCAAAGgtaaggtgggatgaga

M E A K A

Exon 1b (SEQ ID NO: 45/46)

CCATGAGGATTCATAGAAGATGCCCCGCGTCTCGGCGCCTTTGGTGCTGCTTCCTGCGT
M P R V S A P L V L L P A W
GGCTCGTGATGGTCGCCTGCAGCCCGCACTCCTTGAGGATCGgtaagtgtggcccagct
L V M V A C S P H S L R I A

Exon 2 (SEQ ID NO: 47/48)

gaaaccccccccagCTGCTATCTTGACGACCCCATGGAGTGCAGCAGAGGGGAGCGGC
A I L D D P M E C S R G E R L
TCTCCATCACCCCTGGCCAAGAACCGCATCAACCGCGCTCCTGAGAGGCTGGGCAAGGCC
S I T L A K N R I N R A P E R L G K A
AAGGTCGAAGTGGACATCTTTGAGCTTCTCAGAGACAGCGAGTACGAGACTGCAGAAAC
K V E V D I F E L L R D S E Y E T A E T

CAgtacgtagactggg

M

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Figure 16 (SEQ ID NO: 49)

Alternative nucleic acid sequence. Exons 1a-1a'-2-etc.

```

1  gcgtggtagc atgtgcctgt aatcccagtg ctttgggaca ccgaggcagg aggatcactc
61  gagcccagga gtgcgaggct gcagtgcgc tagacttcag gaagaccccc catttctgct
121 ccactcctgg gcttggagaa gagtacagct gctcttgact ggtgggacct tttgctggct
181 aggggtgatg ggagaagcaa gagagggatc cacacacctg cgcttagctt tctatgacct
241 gggcggtatg aggccaaagc tgctatcttg gacgaccca tggagtgcag cagaggggag
301 cggtcttcca tcaccctggc caagaaccgc atcaaccgcg ctctgagag gctgggcaag
361 gccaaggctg agtgagacat ctttgagctt ctcagagaca gcgagtacga gactgcagaa
421 accatgtgtc agatcctccc caagggggtg gtcgctgtcc tcggaccatc gtccagccca
481 gcctccagct ccatcatcag caacatctgt ggagagaagg aggtccctca cttcaaagtg
541 gccccagagg agttcgtcaa gttccagttc cagagattca caaccctgaa cctccacccc
601 agcaacactg acatcagcgt ggctgtagct gggatcctga acttcttcaa ctgcaccacc
661 gcctgcctca tctgtgccaa agcagaatgc cttttaaacc tagagaagct gctccggcaa
721 ttccttatct ccaaggacac gctgtccgtc cgcagtgtgg atgacaccgc ggacccacc
781 ccgctcctca aggagatccg ggacgacaag accgccacca tcatcatcca cgccaacgc
841 tccatgtccc acaccatcct cctgaaggca gccgaacttg ggatgggtgc agctatttac
901 acatacatct tctaatactt ggagttctca ctccagagaa cggacagcct tgtggatgat
961 cgtgtcaaca tcctgggatt ttccattttc aaccaatccc atgctttctt ccaagagttt
1021 gcccagagcc tcaaccagtc ctggcaggag aactgtgacc atgtgccctt cactgggctt
1081 gcgctctcct cggccctgct gtttgatgct gtctatgctg tggtgactgc ggtgcaggaa
1141 ctgaaccgga gccaaagatg cggcgatgaag cccttgctct gcggctcggc ccagatctgg
1201 cagcacggca ccagcctcat gaactacctg cgcagtgtag aattggaagg tcttaccggc
1261 cacattgaat tcaacagcaa aggccagagg tccaactacg ctttgaaaat cttacagttc
1321 acaaggaatg gttttcggca gatcggccag tggcacgtgg cagagggcct cagcatggac
1381 agccacctct atgcctccaa catctcggac actctcttca acaccacctt ggtcgtcacc
1441 accatcctgg aaaaccataa tttaatgctg aaggggaacc accaggagat ggaaggcaat
1501 gaccgctacg agggcttctg tgtggacatg ctcaaggagc tggcagagat cctccgattc
1561 aactacaaga tccgcctggt tggggatggc gtgtacggcg ttcccagggc caacggcacc
1621 tggacgggaa tggtcgggga gctgatcgtc aggaaagcag atctggctgt ggcaggcctc
1681 accattacag ctgaacggga gaaggtgatt gatttctcta agccattcat gactctggga
1741 attagcattc tttaccgcat tcatatggga cgaaaccccg gctattttct cttcctggac
1801 ccattttctc cgggcgtctg gctcttcatg cttctagcct atctggccgt cagctgtgtc
1861 ctcttcctgg tggctcgggt gacgccttac gagtggtaga gccacacccc atgtgccag
1921 ggccggtgca acctcctggt gaaccagtac tccctgggca acagcctctg gtttcgggtc
1981 ggggggttca tgcagcagg ctccaccatc gcccctcgcg ccttatccac ccgctgtgtc
2041 agtggcgtct ggtgggcatt cacgctgatc atcatctcat cctacacggc caacctggca
2101 gccttcctga ccgtgcagcg catggatgtg cccattgagt cagtggatga cctggctgac
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2221 tcccgtctac agacctacca acgcatgtgg aattacatgt attccaagca gccagcgtg
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2521 aaatgggtgg aaggagggaa gtgccccaa gagggaagat acagagctaa aggcctggga
2581 atggagaata ttggtggaat ctttgtgggt cttattttgt gcttaatcgt ggccattttt
2641 atggctatgt tggagttttt atggactctc agacactcag aagcaactga ggtgtccgtc
2701 tgccaggaga tggtgaccga gctgcgcagc attatcctgt gtcaggacag tatccacccc
2761 cgccggcggc gcgcgcagc cccgcgcgcc cggcccccca tccccgagga gcgcgcagcg
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2881 gcgcagagac tggcgcagga ggccgccttg gtggcccgcg gctgcacgca catccgcgtc
2941 tgccccgagt gccgcgcgtt ccagggcctg cgggcacggc cgtcgcgcgc ccgcagcgag
3001 gagagcctgg agtgggagaa aaccaccaac agcagcgagc ccgagtag

```

Figure 17 (SEQ ID NO: 50)

Complete alternative protein sequence

MEAKAAILDDPMECSRGERLSITLAKNRINRAPERLGKAKVEVDIFELLRDSEYETAETMCQ
ILPKGVAVLGPSSSPASSSIISNICGEKEVPHFKVAPEEFVKFQFQFRTTLNLHPSNTDIS
VAVAGILNFFNCTTACLICAKAECLLNLEKLLRQFLISKDTLSVRMLDDTRDPTPLLKEIRD
DKTATIIIIHANASMSHTILLKAAELGMVSAYYTYIFTNLEFSLQRTDSLVD DRVNILGFSIF
NQSHAFFQEFAQSLNQSWQENCDHVPFTGPALSSALLFDAVYAVVTAVQELNRSQEIGVKPL
SCGSAQIWQHGTSLMNYLRMVELEGLTGHEFNSKGQORSNYALKILQFTRNGFRQIGQWHVA
EGLSMDSHLYASNISDTLFTTLVVTILENPLYMLKGNHQEMEGNDRYEGFCVDMLKELAE
ILRFNYKIRLVGDGVYGVPEANGTWTGMVGELIARKADLAVAGLTITAEREKVIDFSKPFMT
LGISILYRIHMGRKPGYFSFLDPFSPGVWLFMLLAYLAVSCVLFLVARLTPYEWYSPHPCAQ
GRCNLLVNQYSLGNSLWFPVGGFMMQQGSTIAPRALSTRCVSGVWVAFTLIIISSYTANLAAF
LTVQRM DVPIESVDDLADQTAIEYGTIHGGSSMTFFQNSRYQTYQRMWNYMYSKQPSVFKS
TEEGIARVLNSNYAFLLESTMNEYRQRCNL TQIGLLDTKGYGIGMPVGSVFRDEFDLAI
LQLOENNRLEILKRKWWEGGKCPKEEDHRAGLGMENIGGIFVVLICGLIVAI FMAMLEFLW
TLRHSEATEVSVCQEMVTELRSIILCQDSIHPRRRRAAVPPRPPIPEERRPRGTATLSNGK
LCGAGEPDQLAQRLAQEAALVARGCTHIRVCPECRRFQGLRARPSPARSEESLEWEKTTNSS
EPE

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Figure 18 (SEQ ID NO: 51)

NPAS3 (NM_022123) nucleic acid sequence (spliceform 1b-3-4etc)

```
1 ccacgcgtcc gacgcccccc acccgggagg ggggagagag gcaaaaagta agagaggaaa
61 aaaaatagca ggaagatggc gccaccaag cccagctttc agcaggatcc ttccaggcga
121 gaacgtttac aagcattgag aaaggagaaa tcccagatg ctgctcgctc ccgccgggga
181 aaagaaaact ttgagttcta tgaattggcc aagttgttgc ctcttctgct agccattacc
241 agccagctcg acaaggcatc catcattcga cttacaatta gctatctgaa aatgagggac
301 ttgctaacc aggggggacc tccgtggaac ttgcgaatgg aaggccctcc acctaacaca
361 tcagtaaaag gtgcacagcg aaggagaagc cccagtgcac tagccattga agtatattgaa
421 gcacatttgg gaagccacat tttgcagtcc ctggatggct ttgtatttgc actaaatcag
481 gaaggaaaat tttgtacat ttccgaaaca gtctccatct acctaggcct ctcaaaagtg
541 gagctgacag gcagcagtggt ctttgactat gtccaccccg gagatcacgt ggagatggct
601 gagcagctgg gcatgaagct cccccctggg cggggtctcc tgtcacaggg cactgctgag
661 gacggagcca gctcagcatc ttctctctct cagtcggaga ccccgagcc agtgagatca
721 accagcccca gtctgctaac cactgacaac actcttgagc gttccttttt catccgaatg
781 aaatctactc tgaccaaacy cgggtgtcac atcaaatacat caggatataa ggtgattcac
841 ataacaggcc ggctacgcct gagagtgtcg ctgtccacag ggaggaccgt cccagccaa
901 atcatgggtc tcgtggttgt tgcgcagtc ttgctcccc ctacgatcaa tgaagtcaga
961 attgactgcc atatgttcgt cactcgagta aatatggacc tcaatatcat ttactgtgaa
1021 aataggatta gtgattatat ggatctgacc cctgtagata tcgtagggaa gagatgctac
1081 cacttcatcc atgctgaaga cgtggagggg atcaggcaca gtcacttgga ctgtctgaat
1141 aagggtcagt gtgtgacaaa gtactatcgc tggatgcaga agaacggagg atatatattg
1201 atacagtcca gtgccaccat agctattaat gccagaatg caaatgaaaa gaatatcatc
1261 tgggtgaatt gtcgcccatc tgccggagaa aacttccgaa tcctcgagga catccgactc tgagtcagac
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1381 tctaaagaca cctcaggtat tacagaggac aacgagaact ccaagtcgga cgagaagggg
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1501 gacaacgaca tgaactgcaa cgacgacggc cacagctcca gtaaccggga cagccgcgac
1561 agcgacgaca gcttcgagca ctccgacttt gagaacccca aggggggcca ggacggcttc
1621 ggtgctctgg gcgcgatgca gatcaagggt gagcgtacg tggagagcga gtcggacctg
1681 cggctgcaga actgcgagtc actcacgtcc gacagcgcca aggactcgga cagcgaggcg
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1801 aaggggcgga gcgccagccg ccggcgccctg tccagcgctg cgagcccagg cggcctggac
1861 gcgggcctgg tggagcccc gcggctgctg tcctccccc acagtgcctc ggtgctcaag
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2101 cacgtggcca tccccgactc ggtcctcacc ccgcccggcg ccgacggcgc ggccgcccgc
2161 aagactcagt tcggcgccct ggccaccgcg gccctggccc ccgtcgccct cgaccgcctg
2221 tcacccccgc tctcggcgtc cccgcgggac aagcaccctg ggaacggcgg gggggcgggg
2281 ggcgggggcg gcggcgcggg gggcgggcgg cccagcgctg ccaactcctt gctgtacact
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2401 agggtgaccg ggaccctggc cgccaccagc acggccgcgc agaggttcta caccacgggc
2461 accatccgct acgcgcccgc cgaggtgacc ctggccatgc agagcaacct gctgcccac
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2581 cccatggaga tgcctacca ccacgtgcac cggctcaaca tgtcaggacc gttcggcggc
2641 gcagtgagcg cagctagcct gacgcagatg cccgccggca acgtgttcac cagggccgag
2701 ggactcttct ccacgtgcc cttccccgtc tacagcaacg gcatccacgc ggcacagact
2761 ctggagcgca aggaggactg aggcgcgcgc cgtcctgggc ccggccaggc ccgcttggg
2821 ggaggcatcg tcggcatatt cgtttagacc tttaattcta gcactttgaa ttcgagcagg
```


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Figure 18, continued

```
2881 tcagcgtctt ctctcgccac gacgggtcccc attccacccc ctctttcttt cacctgactt
2941 attctttcgt gtaaagatat gtttattttt tgccttcaga gggtcagacg accagttgcc
3001 tgccggtttg tcttcttcta aggtgtgtgt tgggttggtt tgctttcctt tgcattctta
3061 ttaagatgtc tttcatgtgt atatgcctct gccatagaat actcagtctt gtggtcaaga
3121 gagttctcaa gtgacaacca ttgggggtttc ttcataaaga tcttgatatg atcaagatgg
3181 aaagagacaa gcataaaciaa tgtgccctgt ttgactaagt caaatgaaat aggggtgggtt
3241 ttgtttctgt tcctaattcc tttaaaaaat agggggaata gtattttaga attttatgca
3301 gaatttaatt ctctttttac ggtaaagatt ttaagatttt cttacttgca cataaaaaata
3361 atttgggttc ttaaaactta tttctggcct gtgactagaa tgtttaaaaa aaaaaaaaaac
3421 cctcgtgc
```

Figure 19 (SEQ ID NO: 52)

NPAS3 protein sequence (spliceform 1b-3-4etc.)

```
MAPTKPSFQQDPSRRERLQALRKEKSRDAARSRRGKENFEFYELAKLLPLPAAITSQLDKAS
IIRLTISYLKMRDFANQGDPPWNLRMEGPPPNTSVKGAQRRRSPSALAIEVFEAHLGSHILQ
SLDGFVFALNQEGKFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMKLPPGR
GLLSQGTAE DGASSASSSSQSETPPEVESTSPSLLTTDNTLERSFFIRMKSTLTGRGVHIKS
SGYKVIHITGRLRLRVSLSHGRTVPSQIMGLVVVAHALPPPTINEVRIDCHMFVTRVNMDLN
IIYCENRISDYMDLTPVDIVGKRCYHFIHAEDVEGIRHSHLDLLNKGQCVTKYYRWMQKNGG
YIWIQSSATIAINAKNANEKNI IWNVYLLSNPEYKDTTPMDIAQLPHLPEKTSESSETSDSES
DSKDTSGITEDNENSKSDEKGNQSENSEDPEPDRKKSGNACDNDMNCNDDGHSSSNPDSRDS
DDSFHSDFFENPKAGEDGFGALGAMQIKVERYVESESDLRLQNCESLTSDSAKDSDSAGEAG
AQASSKHQKRKKRRKRQKGSASRRRLSSASSPGGLDAGLVEPPRLSSPNSASVLKIKTEI
SEPINFDNDSSIWNYPNREISRNEPYSMTKPPSSEHFPSPOGGGGGGGGGGGLHVAIPDS
VLTPPGADGAAARKTQFGASATAALAPVASDPLSPPLSASPRDKHPGNGGGGGGGGGGAGGG
GPSASNSLLYTGDLEALQRLQAGNVVLPLVHRVTGTLAATSTAAQRVYTTGTIRYAPAEVTL
AMQSNLLPNAHAVNFVDVNSPGFGLDPKTPMEMLYHHVHRLNMSGPFGGAVSAASLTQMPAG
NVFTTAEGLFSTLPFPVYSNGIHAAQTLERKED
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Figure 20 (SEQ ID NO: 53)

NPAS3 nucleic acid sequence (spliceform incorporating exons 1a-2-3-4etc) similar to mouse cDNA with accession number NM_013780)

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1  ATGGGGAGGG CCGGCGCCGC GGCCAACGGC ACCCCGCAGA ACGTCCAGGG CATCACCTCC
61  TACCAGCAGC GAATAACTGC CCAGCATCCT CTGCCCCAACC AATCAGAATG TAGGAAAAATC
121 TACAGATATG ACGGAATCTA CTGTGAATCT ACCTACCAGA ATTTACAAGC ATTGAGAAAAG
181 GAGAAATCCC GAGATGCTGC TCGTCCCGC CGGGGAAAAG AAAACTTTGA GTTCTATGAA
241 TTGGCCAAGT TGTTGCCCTCT TCCTGCAGCC ATTACCAGCC AGCTCGACAA GGCATCCATC
301 ATTGCACTTA CAATTAGCTA TCTGAAAATG AGGGACTTTG CTAACCAGGG GGACCCTCCG
361 TGGAACCTTG GAATGGAAGG CCGTCCACCT AACACATCAG TAAAAGGTGC ACAGCGAAGG
421 AGAAGCCCCA GTGCACTAGC CATTGAAGTA TTTGAAGCAC ATTTGGGAAG CCACATTTTG
481 CAGTCCCTGG ATGGCTTTGT ATTTGCACTA AATCAGGAAG GAAAATTTTT GTACATTTCC
541 GAAACAGTCT CCATCTACCT AGGCCTCTCA CAAGTGGAGC TGACAGGCAG CAGTGTCTTT
601 GACTATGTCC ACCCCGAGAG TCACGTGGAG ATGGCTGAGC AGCTGGGCAT GAAGCTCCCC
661 CCTGGGCGGG GTCTCCTGTC ACAGGGCACT GCTGAGGACG GAGCCAGCTC AGCATCTTCC
721 TCCTCTCAGT CGGAGACCCC CGAGCCAGTG GAGTCAACCA GCCCCAGTCT GCTAACCACT
781 GACAACACTC TTGAGCGTTC CTTTTTCATC CGAATGAAAT CTACTCTGAC CAAACGCGGT
841 GTGCACATCA AATCATCAGG ATATAAGGTG ATTCACATAA CAGGCCGGCT ACGCCTGAGA
901 GTGTCGCTGT CCCACGGGAG GACCGTCCCC AGCCAAATCA TGGGTCTCGT GGTGTGTGCG
961 CATGCCCTGC CTCCCCCTAC GATCAATGAA GTCAGAATTG ACTGCCATAT GTTCGTCACT
1021 CGAGTAAATA TGGACCTCAA TATCATTTAC TGTGAAAATA GGATTAGTGA TTATATGGAT
1081 CTGACCCCTG TAGATATCGT AGGGAAGAGA TGCTACCACT TCATCCATGC TGAAGACGTG
1141 GAGGGCATCA GGCACAGTCA CTTGGACTTG CTGAATAAGG GTCAGTGTGT GACAAAGTAC
1201 TATCGCTGGA TGCAGAAGAA CGGAGGATAT ATTTGGATAC AGTCCAGTGC CACCATAGCT
1261 ATTAATGCCA AGAATGCAAA TGAAAAGAAT ATCATCTGGG TGAATTACCT TCTTAGCAAT
1321 CCTGAGTACA AGGACACACC CATGGACATC GCACAGCTCC CCCATCTGCC GGAGAAAAC
1381 TCCGAATCCT CGGAGACATC CGACTCTGAG TCAGACTCTA AAGACACCTC AGGTATTACA
1441 GAGGACAACG AGAAGTCCAA GTCCGACGAG AAGGGGAACC AGTCCGAGAA CAGCGAAGAC
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1621 GACTTTGAGA ACCCAAGGC GGGCGAGGAC GGCTTCGGTG CTCTGGGCGC GATGCAGATC
1681 AAGGTGGAGC GCTACGTGGA GAGCGAGTCG GACCTGCGGC TGCAGAACTG CGAGTCACTC
1741 ACGTCCGACA GCGCCAAGGA CTCGGACAGC GCAGGCGAGG CGGGCGCGCA GGCTCCAGC
1801 AAGCACCAGA AGCGCAAGAA AAGGCGGAAA CGGCAAAAGG GCGGCAGCGC CAGCCGCCGG
1861 CGCCTGTCCA GCGCGTCGAG CCCAGGCGGG CTGGACGCGG GCCTGGTGGA GCCCCCGCG
1921 CTGCTGTCCT CCCCCAACAG TGCCTCGGTG ATCAAGATCA AGACGGAGAT CTCAGAACCC
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2041 AACGAGTCCC CCTACAGCAT GACCAAGCCC CCCAGCTCTG AGCACTTCCC GTCCCCGCG
2101 GGCGGCGGCG GTGGGGGTGG CGGTGGCGGG GGGCTGCACG TGGCCATTCC CGACTCGGTC
2161 CTCACCCCGC CCGGCGCCGA CGGCGCGGCC GCCCGCAAGA CTCAGTTCGG CGCCTCGGCC
2221 ACCGCGGCCC TGGCCCCCGT CGCCTCCGAC CCGCTGTCAC CCCCGCTCTC GGCGTCCCCG
2281 CGGGACAAGC ACCCCGGGAA CGGCGGCGGG GGCGGGGGCG GGGGCGGCGG CGCGGGGGGG
2341 GGCGGCCCCA GCGCGTCCAA CTCCTTGCTG TACACTGGGG ACCTGGAGGG GCTGCAGAGG
2401 TTGCAGGCGG GCAACGTCGT GCTCCCGCTG GTGCACAGGG TGACCGGGAC CCTGGCCGCC
2461 ACCAGCAGCG CCGCGCAGAG GGTCTACACC ACGGGCACCA TCCGCTACGC GCCCGCCGAG
2521 GTGACCTTGG CCATGCAGAG CAACCTGCTG CCAACGCGC ACGCTGTAA CTTCGTGGAC
2581 GTTAACAGCC CCGGCTTTGG CCTCGACCCC AAGACGCCCA TGGAGATGCT CTACCACCAC
2641 GTGCACCGGC TCAACATGTC AGGACCGTTC GGCGGCGCAG TGAGCGCAGC TAGCCTGACG
2701 CAGATGCCCC CCGGCAACGT GTTCAACACG GCCGAGGGAC TCTTCTCCAC GCTGCCCTTC
2761 CCCGTCTACA GCAACGGCAT CCACGCGGCA CAGACTCTGG AGCGCAAGGA GGACTGAGGC
2821 GCCGCCCGTC CTGGGCCCCG CCAGGCCCCG CTTGGAGGAG GCATCGTCGG CATTTTCGTT

```

Figure 20, continued

2881 TAGACCTTTA ATTCTAGCAC TTTGAATTCG AGCAGGTCAG CGTCTTCTCT CGCCACGACG
2941 GTCCCCATTC CACCCCCTCT T

Figure 21 (SEQ ID NO: 54)

NPAS3 protein sequence of spliceform incorporating exons 1a-2-3-4etc.

MGRAGAAANGTPQNVQGITSYQQRITAQHPLPNQSECRKIYRYDGIYCESTYQNLQALRKEK
SRDAARSRRGKENFEFYELAKLLPLPAAITSQLDKASIIRLTISYLMRDFANQGDPPWNLR
MEGPPPNTSVKGAQRRRSPSALAIEVFEAHLGSHILQSLDGFVFALNQEGKFLYISETVSIY
LGLSQVELTGSSVFDYVHPGDHVEMAEQLGMKLPPGRGLLSQGTAEKGASSASSSSQSETPE
PVESTSPSLLTDTNLTSLERSFFIRMKSTLTKRGVHIKSSGYKVIHITGRLRLRVSLSHGRTVP
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NSEDPEPDRKKSGNACDNDMNCNDDGHSSSNPDSRDSDDSFHSDFENPKAGEDGFGALGAM
QIKVERYVESESDLRLQNCESLTSDSAKSDSAGEAGAQAASSKHQKRKKRRKRQKGGASARR
RLSSASSPGGLDAGLVEPPRLLSPPNSASVLKIKTEISEPINFDNDSSIWNYPNREISRNE
SPYSMTKPPSSEHFPSPOGGGGGGGGGGGLHVAIPDSVLTTPGADGAAARKTQFGASATAAL
APVASDPLSPPLSASPRDKHPGNGGGGGGGGGGAGGGGPPSASNSLLYTGDLEALQRLQAGNV
VLPLVHRVTGTLAATSTAAQRVYTTGTIRYAPAEVTLAMQSNLLPNAHAVNFVDVNSPGFGL
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QTLERKED

Figure 22

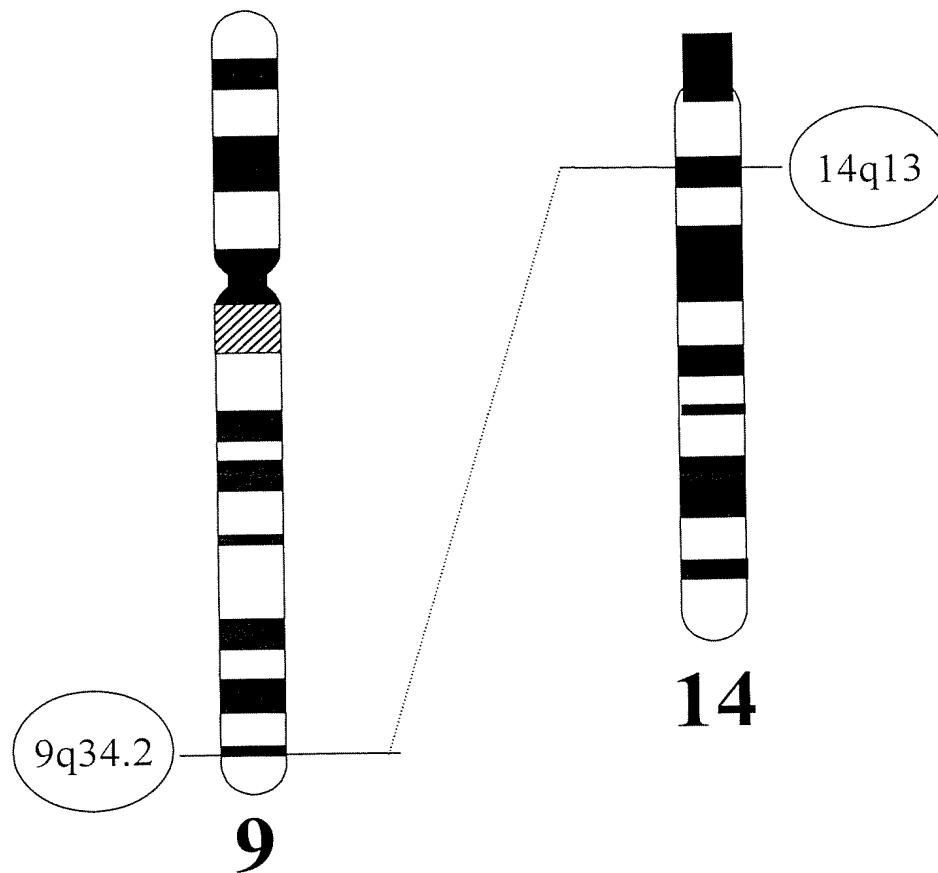


Figure 23

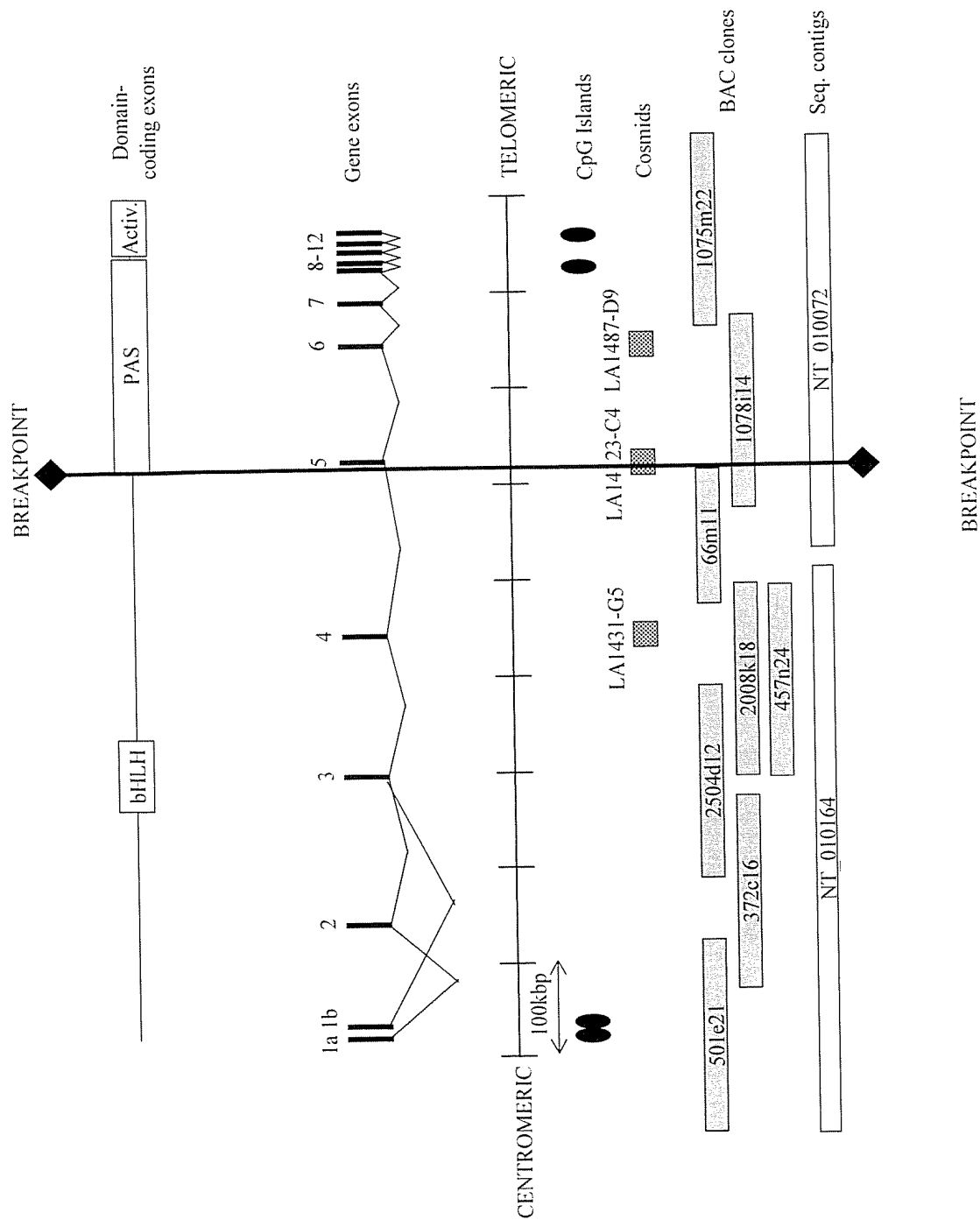
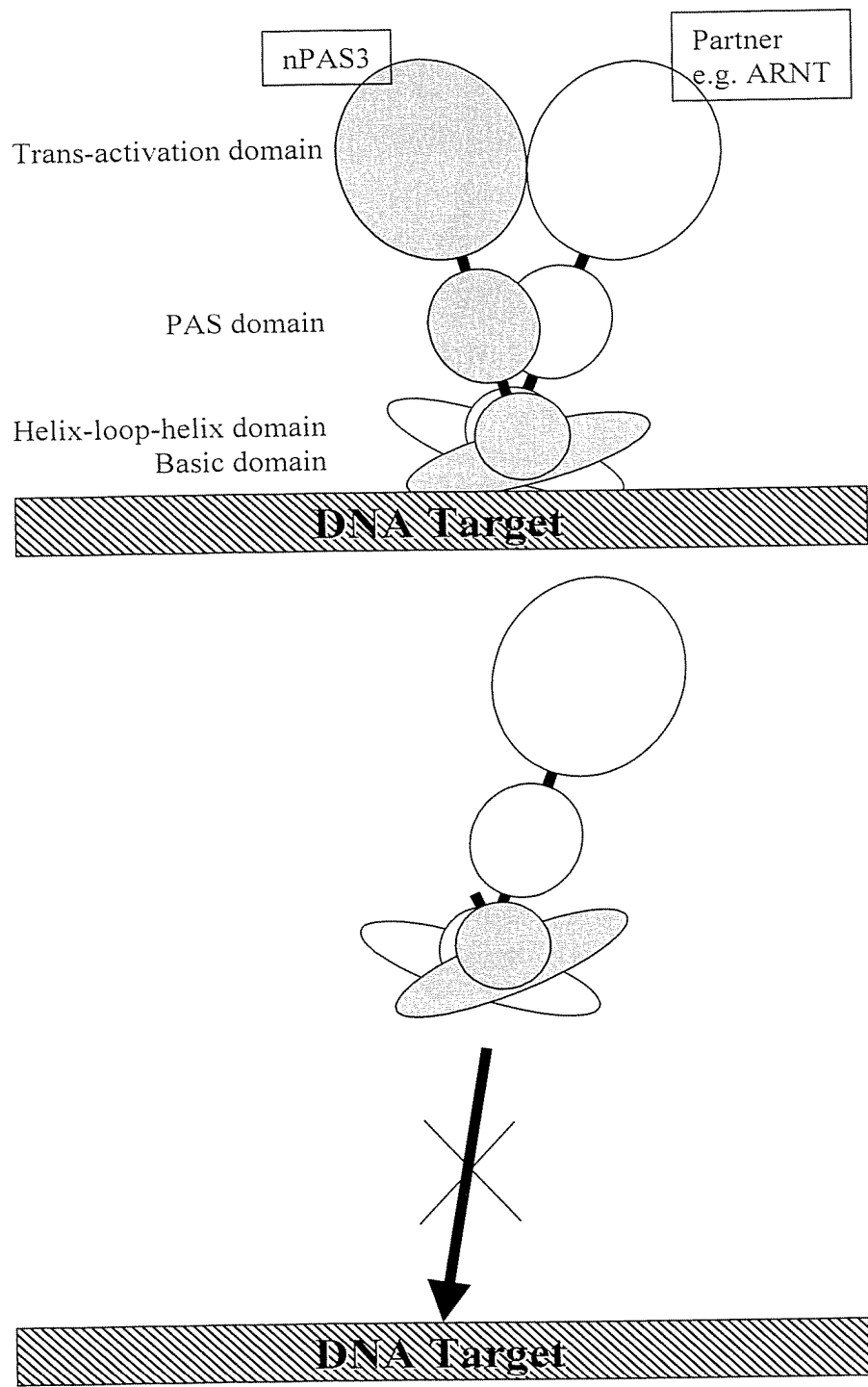


Figure 24



REPLACEMENT SHEET

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Figure 25 (SEQ ID NO: 55)

PDE4B1 (acc. L20966) Nucleic acid sequence

```
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61  agcctgaggt  attaaaaagt  gtcagcaaac  tgcattgaat  aacagacatc  ctaagagggg
121  atattttcca  cctctataat  gaagaaaagc  aggagtgtga  tgacgggtgat  ggctgatgat
181  aatgttaaag  attattttga  atgtagcttg  agtaaatcct  acagttcttc  cagtaacaca
241  cttgggatcg  acctctggag  agggagaagg  tgttgctcag  gaaacttaca  gttaccacca
301  ctgtctcaaa  gacagagtga  aagggcaagg  actcctgagg  gagatggtat  ttccaggccg
361  accacactgc  ctttgacaac  gcttccaagc  attgctatta  caactgtaag  ccaggagtgc
421  tttgatgtgg  aaaatggccc  ttccccaggt  cggagtccac  tggatcccca  ggccagctct
481  tccgctgggc  tgg tacttca  cgccaccttt  cctgggcaca  gccagcgcag  agagtcatth
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661  agcttgcgaa  gtgtgagaaa  caacttcact  atactgacaa  accttcattg  tacatctaac
721  aagaggtccc  cagctgctag  tagcaatgga  aacgctggag  gaattagact  ggtgtttaga  ccagctagag
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1261  agagacctcc  taaagacatt  tgacgtggca  tatcacaaca  gcctgcacgc  tgctgatgta
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1501  aatcagtttc  tcatcaacac  aaattcagaa  cttgctttga  tgtataatga  tgaatctgtg
1561  ttggaaaatc  atcaccttgc  tgtgggtttc  aaactgctgc  aagaagaaca  ctgtgacatc
1621  ttcatgaatc  tcaccaagaa  gcagcgtcag  aactcagga  agatggttat  tgacatgggt
1681  ttagcaactg  atatgtctaa  acatatgagc  ctgctggcag  acctgaagac  aatggtagaa
1741  acgaagaaag  ttacaagttc  aggcgttctc  ctctagacac  ccaccaagtc  cttggaattg
1801  gtctttcgca  acatggtaca  ctgtgcagac  ctctagacac  ccaccaagtc  cttggaattg
1861  tatcggaat  ggacagaccg  catcatggag  gaatttttcc  agcagggaga  caaagagcgg
1921  gagaggggaa  tggaaattag  cccaatgtgt  gataaacaca  cagcttctgt  ggaaaaatcc
1981  caggttggtt  tcatcgacta  cattgtccat  ccattgtggg  agacatgggc  agatttggtg
2041  cagcctgatg  ctacggacat  tctcgatacc  ttagaagata  acaggaactg  gtatcagagc
2101  atgatacctc  aaagtccctc  accaccactg  gacgagcaga  acagggactg  ccagggtctg
2161  atggagaagt  ttcagtttga  actgactctc  gatgaggaag  attctgaagg  acctgagaag
2221  gagggagagg  gacacagcta  tttcagcagc  acaaagacgc  tttgtgtgat  tgatccagaa
2281  aacagagatt  ccctgggaga  gactgcata  gacattgcaa  cagaagacaa  gtccccctg
2341  gatacataat  cccctctctc  ctgtggagat  gaacattcta  tccttgatga  gcatgccagc
2401  tatgtggtag  ggccagccca  ccatgggggc  caagacctgc  acaggacaag  ggccacctgg
2461  cttttcagtt  acctgagttt  ggagtcagaa  agcaagacca  ggaagcaaat  agcagctcag
2521  gaaatcccac  gggtgacttg  ccttgatggc  aagcttggtg  gagagggctg  aagctgttgc
2581  tgggggcccga  ttctgatcaa  gacacatggc  ttgaaaatgg  aagacacaaa  actgagagat
2641  cattctgcac  taagtttcgg  gaacttatcc  ccgacagtga  ctgaactcac  tgactaataa
2701  cttcattht  gaatcttctc  acttgctcct  ttgtctgcca  acctgtgtgc  cttttttgta
2761  aaacattht  atgtcttht  aatgcctgtt  gaatacctgg  agtttagtat  caacttctac
2821  acagataagc  tttcaaagtt  gacaaacttt  tttgactctt  tctggaaaag  ggaaagaaaa
2881  tagtcttct  tctttcttgg  gcaatatcct  tcactttact  acagttactt  ttgcaaacag
2941  acagaaagga  tacacttcta  accacattht  acttccttcc  cctgttgtcc  agtccaactc
3001  cacagtcact  cttaaaactt  ctctctgttt  gcctgcctcc  aacagtactt  ttaacttht
3061  gctgtaaaaca  gaataaaatt  gaacaaatta  gggggtagaa  aggagcagtg  gtgtcgttca
3121  ccgtgagagt  ctgcatagaa  ctcagcagtg  tgccctgctg  tgtcttgagc  cctgcaatgc
3181  ggccgc
```

Figure 26 (SEQ ID NO: 56)

PDE4B1 Protein sequence

MKKSRSVMTVMADDNVKDYFECSLSKSYSSSSNTLGIDLWRGRRCCSGNLQLPPLSQRQSER
ARTPEGDGISRPTTLPLTTLPISIAITTVSQECFDVENGPSPGRSPLDPQASSSAGLVLHATF
PGHSQRRESFLYRSDSDYDLSPKAMSRNSSLPSEQHGDDLIVTPFAQVLASLRSVRNNFTIL
TNLHGTSNKRSPAASQPPVSRVNPQEESYQKLAMETLEELDWCLDQLETIQTYRSVSEMASN
KFKRMLNRELTHLSEMSRSGNQVSEYISNTFLDKQNDVEIPSPTQKDREKKKKQQLMTQISG
VKKLMHSSSLNNTSISRFGVNTENEDHLAKELEDLNKWGLNIFNVAGYSHNRPLTCIMYAI
QERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPALDAVFTDL
EILAAIFAAAIHDVDHPGVSNOFLINTNSEALMYNDESVLENHHLAVGFKLLQEEHCDIFM
NLTKKQROTTLRKMVIDMVLATDMSKHMSLLADLKTMTVETKKVTSSGVLLLDNYTDRIQVLRN
MVHCADLSNPTKSLELYRQWTDRIEEMFFQOGDKERERGMEISPMCDKHTASVEKSQVGFID
YIVHPLWETWADLVQPDADILDITLEDNRNWDYQSMIPQSPSPPLDEQNRDCQGLMEKFQFEL
TLDEEDSEGPEKEGEGHSYFSSTKTLCVIDPENRDSLGETDIDIATEDKSPVDT

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Figure 27 (SEQ ID NO: 57)

PDE4B3 (acc. U85048) Nucleic acid sequence

```
1 atgacagcaa aagattcttc aaaggaactt actgcttctg aacctgaggt ttgcataaag
61 acttttcaagg agcaaatgca tttagaactt gagcttccga gattaccagg aaacagacct
121 acatctccta aaattttctcc acgcagttca ccaaggaact caccatgctt tttcagaaag
181 ttactgggtga ataaaagcat tcggcagcgt cgtcgcttca ctgtggctca tacatgcttt
241 gatgtggaaa atggcccttc cccaggctcg agtccactgg atccccaggc cagctcttcc
301 gctgggctgg tacttcacgc cacctttcct gggcacagcc agcgcagaga gtcatttctc
361 tacagatcag acagcgacta tgacttgatc ccaaaggcga tgtcgagaaa ctcttctctt
421 ccaagcgagc aacacggcga tgacttgatt gtaactcctt ttgcccaggc ccttgccagc
481 ttgcgaagtg tgagaaacaa cttcactata ctgacaaacc ttcattggtac atctaacaag
541 aggtccccag ctgctagtca gcctcctgtc tccagagtca acccaacaaga agaattctat
601 caaaaattag caatggaaac gctggaggaa ttagactggg gtttagacca gctagagacc
661 atacagacct accggtctgt cagtgaagtg gcttctaaca agttcaaaag aatgctgaac
721 cgggagctga cacacctctc agagatgagc cgatcaggga accagggtgtc tgaatacatt
781 tcaaatactt tcttagacaa gcagaatgat gtggagatcc catctcctac ccagaaagac
841 agggagaaaa agaaaaagca gcagctcatg acccagataa gtggagtga gaaattaatg
901 catagttaa gcctaaacaa tacaagcatc tcacgctttg gagtcaacac tgaaaatgaa
961 gatcacctgg ccaaggagct ggaagacctg aacaaatggg gtcttaacat ctttaattgt
1021 gctggatatt ctcaaatag acccctaaca tgcacatgt atgctatatt ccaggaaaga
1081 gacctcctaa agacattcag aatctcatct gacacattta taacctacat gatgacttta
1141 gaagaccatt accattctga cgtggcatat cacaacagcc tgcacgctgc tgatgtagcc
1201 cagtcgaccc atgttctcct ttctacacca gcattagacg ctgtcttcac agatttggag
1261 atcctggctg ccatttttgc agctgccatc catgacgttg atcatcctgg agtctccaat
1321 cagtttctca tcaacacaaa ttcagaactt gctttgatgt ataattatga atctgtgttg
1381 gaaaatcatc accttgctgt gggtttcaaa ctgctgcaag aagaacactg tgacatcttc
1441 atgaatctca ccaagaagca gcgtcagaca ctgaggaaga tggttattga catggtgtta
1501 gcaactgata tgtctaaaca tatgagcctg ctggcagacc tgaagacaat ggtagaaacg
1561 aagaaagtta caagttcagg cgttcttctc ctgacaaact ataccgatcg cattcaggctc
1621 cttcgcaaca tgggtacactg tgcagacctg agcaacccca ccaagtcctt ggaattgtat
1681 cggcaatgga cagaccgcat catggaggaa tttttccagc agggagacaa agagcgggag
1741 aggggaatgg aaattagccc aatgtgtgat aaacacacag cttctgtgga aaaatcccag
1801 gttggtttca tcgactacat tgtccatcca ttgtgggaga catgggcaga tttggtacag
1861 cctgatgctc aggacattct cgatacctta gaagataaca ggaactggta tcagagcatg
1921 atacctcaaa gtccctcacc accactggac gagcagaaca gggactgcca gggctctgat
1981 gagaagtttc agtttgaact gactctcgat gaggaagatt ctgaaggacc tgagaaggag
2041 ggagagggac acagctatct cagcagcaca aagacgcttt gtgtgattga tccagaaaac
2101 agagattccc tgggagagac tgacatagac attgcaacag aagacaagtc ccccgaggat
2161 aca
```

Figure 28 (SEQ ID NO: 58)

PDE4B3 Protein sequence

MTAKDSSKELTASEPEVCIKTFKEQMHLELELPRLPGNRPTSPKISPRSSPRNSPCFFRKLL
VNKSIRQRRRFTVAHTCFDVENGPSPGRSPLDPQASSSAGLVLHATFPGHSORRESFLYRSD
SDYDLSPKAMSRNSSLPSEQHGDDLIVTPFAQVLASLRSVRNNFTILTNLHGTSNKRSPAAS
QPPVSRVNPQEESYQKLAMETLEELDWCLDQLETTIQTYSVSEMASNKFKRMLNRELTHLSE
MSRSGNQVSEYISNTFLDKQNDVEIPSPTQKDREKKKKQQLMTQISGVKKLMHSSSLNNTSI
SRFGVNTENEDHLAKELEDLNKWGLNIFNVAGYSHNRPLTCIMYAIQERDLLKTFRISSDT
FITYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVD
HPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLLQEEHCDIFMNLTKKQROTTLRKMVI
DMVLATDMSKHMSLLADLKTMTVETKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLE
LYRQWTDRIEIEFFQQGDKERERGMESISPMCDKHTASVEKSQVGFIDYIVHPLWETWADLVQ
PDAQDILDTLEDNRNWKYQSMIPQSPSPPLDEQNRDCQGLMEKFQFELTLDEEDSEGPEKEGE
GHSYFSSTKTLCTVIDPENRDSLGETDIDIATEDKSPVDT

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Figure 29 (SEQ ID NO: 59)

PDE4B2 (acc. NM_002600) Nucleic acid sequence

```
1 gaattcctcc tctcttcacc ccgttagctg ttttcaatgt aatgctgccg tccttctctt
61 gcactgcctt ctgcgctaac acctccattc ctgtttataa ccgtgtattt attacttaat
121 gtatataatg taatgttttg taagtattta atttatataat ctaacattgc ctgccaatgg
181 tgggtgttaaa tttgtgtaga aaactctgcc taagagttac gactttttct tgtaatgttt
241 tgtattgtgt attatataac ccaaacgtca cttagtagag acatatggcc cccttggcag
301 agaggacagg ggtgggcttt tgttcaaagg gtctgccctt tccctgcctg agttgctact
361 tctgcacaac ccctttatga accagttttc acccgaattt tgactgtttc atttagaaga
421 aaagcaaaat gagaaaaagc tttcctcatt tctccttgag atggcaaagc actcagaaat
481 gacatcacat accctaaaga accttgggat gactaaggca gagagagtct gagaaaactc
541 tttggtgctt ctgcctttag ttttaggaca ctttatgca gatgagctta taagagaccg
601 ttccttcctc cttcttcctc agaggaaagt tcttggtaga tcaccgacac ctcatccagg
661 cggggggttg gggggaaact tggcaccagc catcccaggc agagcaccac tgtgatttgt
721 tctcctggtg gagagagctg gaaggaagga gccagcgtgc aaataatgaa ggagcacggg
781 ggcaccttca gtagcaccgg aatcagcggg ggtagcggtg actctgctat ggacagcctg
841 cagccgctcc agcctaacta catgcctgtg tgtttgtttg cagaagaatc ttatcaaaaa
901 ttagcaatgg aaacgctgga ggaattagac tgggtgtttg accagctaga gaccatacag
961 acctaccggt ctgtcagtga gatggcttct aacaagttca aaagaatgct gaaccgggag
1021 ctgacacacc tctcagagat gagcggatca gggaaaccagg tgtctgaata catttcaaat
1081 acttttcttag acaagcagaa tcatgtggag atcccatctc ctaccagaa agacagggag
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1201 tcaagcctaa acaatacaag catctcacgc tttggagtca aactgaaaa tgaagatcac
1261 ctggccaagg agctggaaga cctgaacaaa tggggcttta acatctttaa tgtggctgga
1321 tattctcaca atagaccctt aacatgcatt atgtatgcta tattccagga aagagacctc
1381 ctaaagacat tcagaatctc atctgacaca ttataacctt acatgatgac tttagaagac
1441 cattaccatt ctgacgtggc atatcacaac agcctgcacg ctgctgatgt agcccagtcg
1501 acccatgttc tcctttctac accagcatta gacgtgtctt tcacagattt ggagatcctg
1561 gctgccattt ttgcagctgc catccatgac gttgatcatc ctggagtctc caatcagttt
1621 ctcatcaaca caaattcaga acttgccttg atgtataatg atgaatctgt gttggaaaat
1681 catcaccttg ctgtgggttt caaactgctg caagaagaac actgtgacat cttcatgaat
1741 ctcaccaaga agcagcgtca gacactcagg aagatggtta ttgacatggt gttagcaact
1801 gatattgtct aacatatgag cctgctggca gacctgaaga caatggtaga aacgaagaaa
1861 gttacaagtt caggcgttct tctcctagac aactataccg atcgattca ggtccttcgc
1921 aacatggtac actgtgcaga cctgagcaac cccaccaagt ccttgggaatt gtatcggcaa
1981 tggacagacc gcatcatgga ggaatttttc cagcagggag acaaagagcg ggagagggga
2041 atggaaatta gcccaatgtg tgataaacac acagcttctg tggaaaaatc ccaggttggt
2101 ttcategact acattgtcca tccattgtgg gagacatggg cagatttggt acagcctgat
2161 gctcaggaca ttctcgatac cttagaagat aacaggaact ggtatcagag catgatacct
2221 caaagtcctt caccaccact ggacgagcag aacagggact gccaggtctt gatggagaag
2281 tttcagtttg aactgactct cgataggaa gattctgaag gacctgagaa ggagggagag
2341 ggacacagct atttcagcag cacaagacg ctttgtgtga ttgatccaga aaacagagat
2401 tccctgggag agactgacat agacattgca acagaagaca agtccccctg ggatacataa
2461 tccccctctc cctgtggaga tgaacattct atccttgatg agcatgccag ctatgtggta
2521 gggccagccc accatggggg ccaagacctg cacaggacaa gggccacctg gcctttcagt
2581 tacttgagtt tggagtcaga aagcaagacc aggaagcaaa tagcagctca ggaatccca
2641 cggttgactt gccttgatgg caagcttggg ggagagggct gaagctgttg ctgggggccc
2701 attctgatca agacacatgg cttgaaaatg gaagacacaa aactgagaga tcattctgca
2761 ctaagtcttc ggaacttatc cccgacagtg actgaactca ctgactaata acttcattta
2821 tgaatcttct cacttgtccc tttgtctgcc aacctgtgtg ccttttttgt aaaacatttt
2881 catgtcttta aaatgcctgt tgaataacct gagtttagta tcaacttcta cacagataag
2941 ctttcaaagt tgacaaaact ttttgactct ttctggaaaa gggaaagaaa atagtcttcc
```

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Figure 29, continued

```

3001 ttctttcttg ggcaatatcc ttacttttac tacagttact tttgcaaaca gacagaaagg
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3121 tcttaaaaact tctctctgtt tgcctgcctc caacagtact tttaactttt tgctgtaaac
3181 agaataaaaat tgaacaaaatt agggggtaga aaggagcagt ggtgtcgttc accgtgagag
3241 tctgcataga actcagcagt gtgccctgct gtgtcttgga ccctgcccc caccaggagt
3301 gctacagtcc ctggccctgc ttcccatcct cctctcttca ccccgtttagc tgttttcaat
3361 gtaatgctgc cgtccttctc ttgcactgcc ttctgcgcta acacctccat tcctgtttat
3421 aaccgtgtat ttattactta atgtatataa tgtaatgttt tgtaagttat taatttatat
3481 atctaacatt gcctgccaat ggtggtgtta aatttggtga gaaaactctg cctaagagtt
3541 acgacttttt cttgtaatgt tttgtattgt gtattatata acccaaactg cacttagtag
3601 agacatatgg ccccttggc agagaggaca ggggtgggct tttgttcaaa gggctctgcc
3661 tttccctgcc tgagttgcta cttctgcaca acccctttat gaaccagttt tggaacaat
3721 attctcacat tagatactaa atggtttata ctgagtcctt tacttttgta tagcttgata
3781 ggggcagggg caatgggatg tagtttttac ccaggttcta tccaaatcta tggggcatg
3841 agttgggtta taactggatc ctactatcat tgtggctttg gttcaaaagg aaacactaca
3901 tttgctcaca gatgattctt ctgattcttc tgaatgctcc cgaactactg actttgaaga
3961 ggtagcctcc tgctgcat taagcaggaa tgtcatgttc cagttcatta caaaagaaaa
4021 caataaaaaca atgtgaattt ttataataaa aaaaaaaaaa aggaattc

```

Figure 30 (SEQ ID NO: 60)

PDE4B2 Protein sequence

```

MKEHGGTFSSSTGISGGSGDSAMDSLQPLQPNYMPVCLFAEESYQKLAMETLEELDWCLDQLE
TIQTYRSVSEMASNKFKRMLNRELTHLSEMSRSGNQVSEYISNTFLDKQNDVEIPSPTQKDR
EKKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKELEDLNKWGLNIFNVAGY
SHNRPLTCIMYAIQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADVAQSTHV
LLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAV
GFKLLQEEHCDIFMNLTKKQROT LRKMVIDMVLATDMSKHMSLLADLKT MVETKKVTSSGVL
LLDNYTDRIQVLRNMVHCADLSNPTKSLELYRQWTD RIMEEFFQQGDKERERGM EISPMCDK
HTASVEKSQVGFIDYIVHPLWETWADLVQPD AQDILD TLEDNRNWYQSMIPQSPSPPLDEQN
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KSPVDT

```

Figure 31

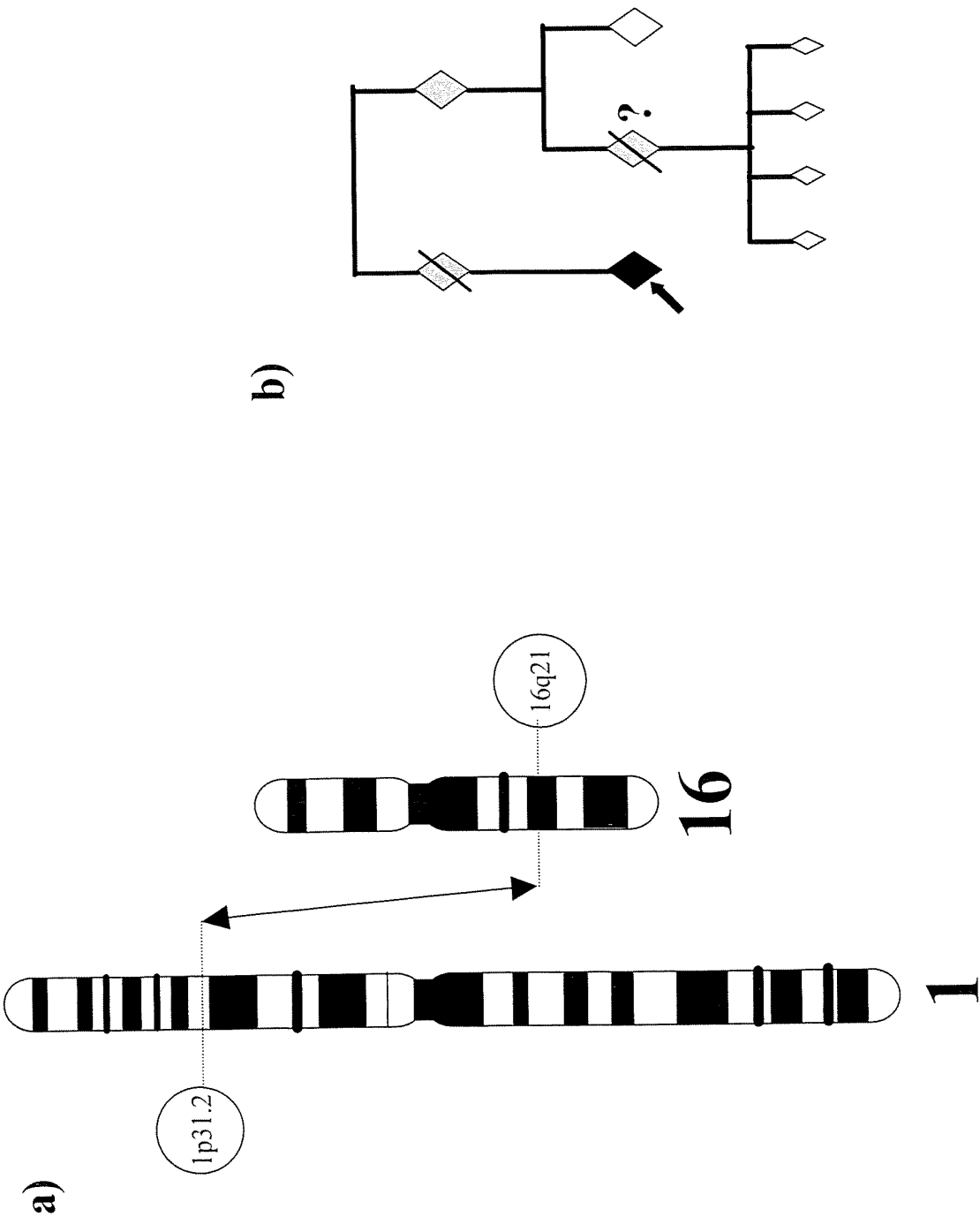


Figure 32

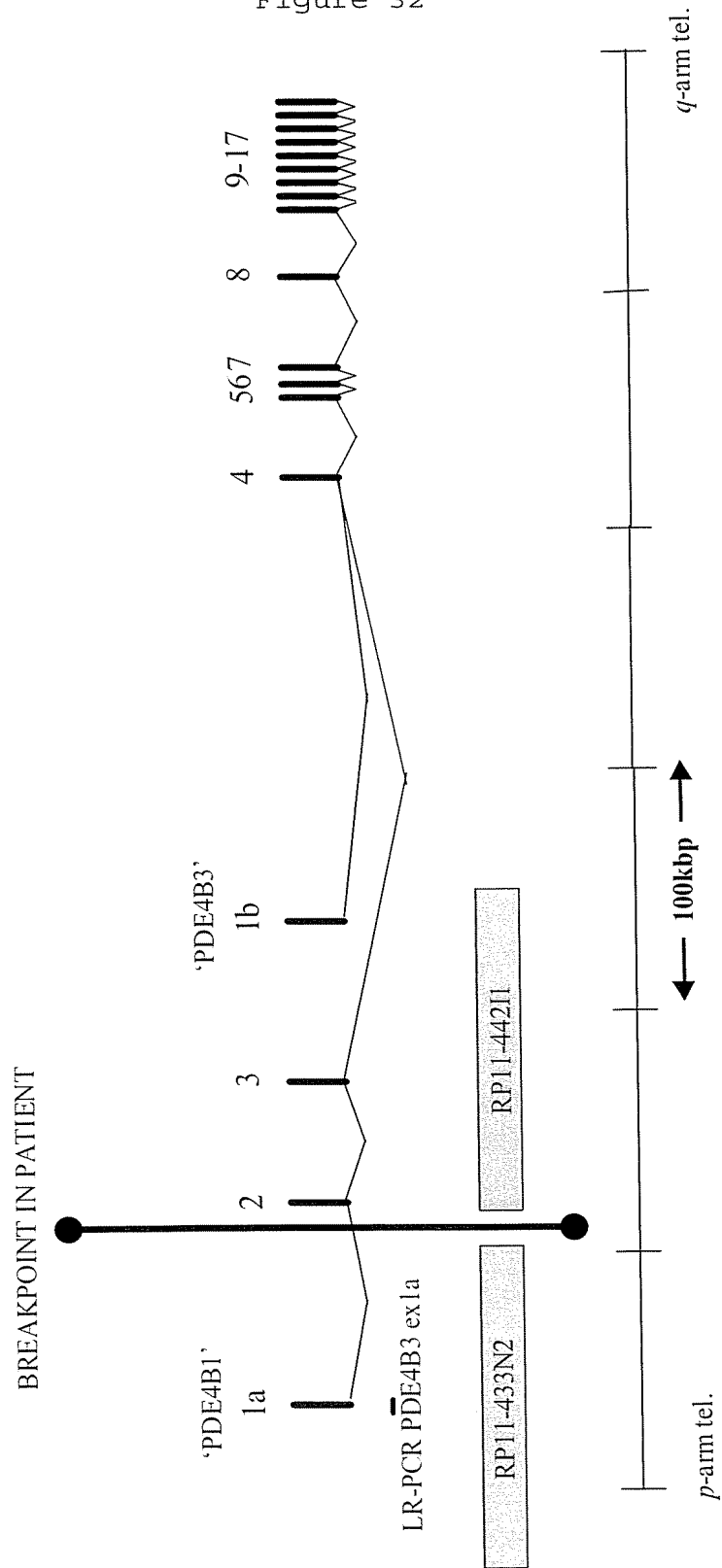


FIGURE 33

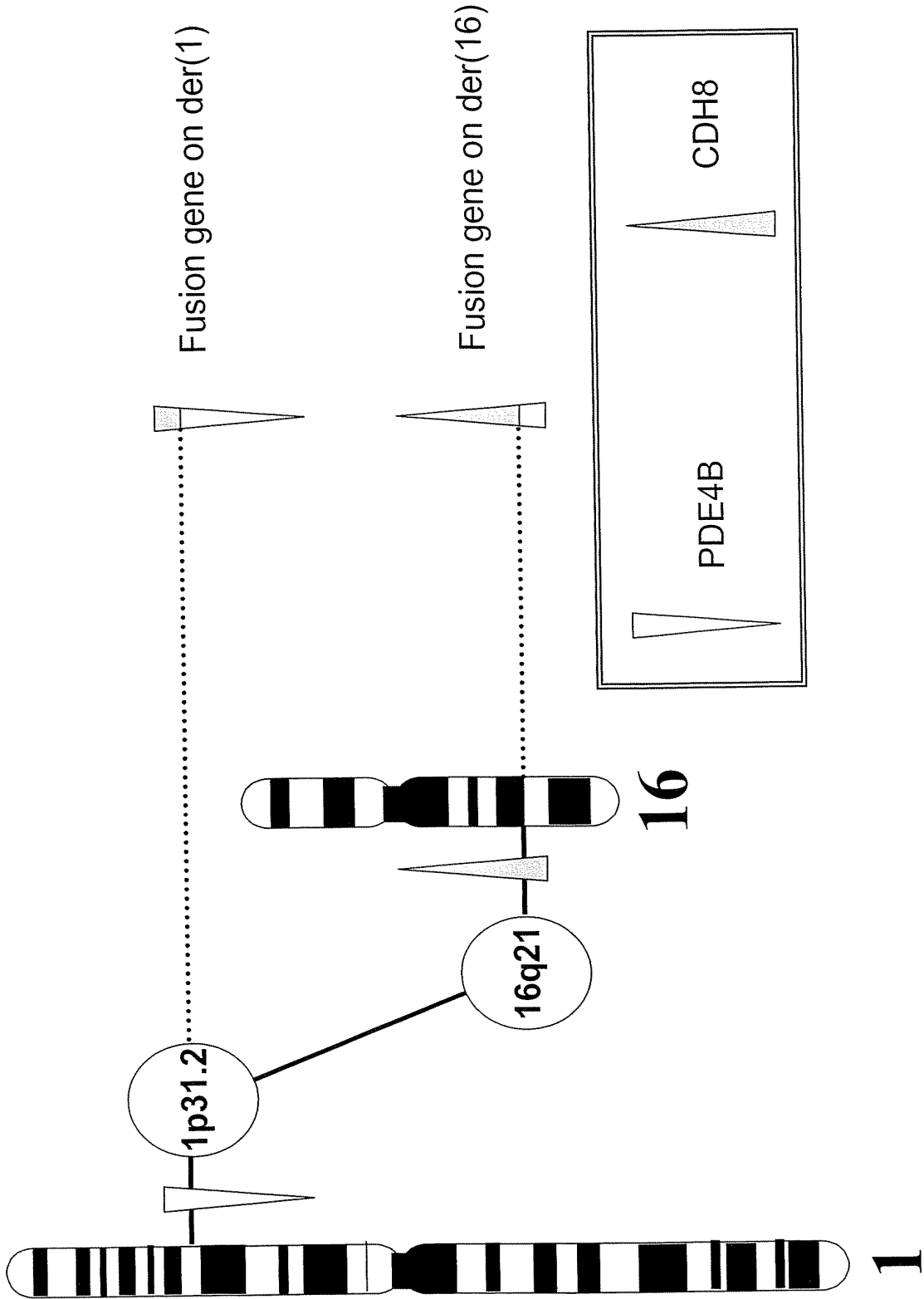
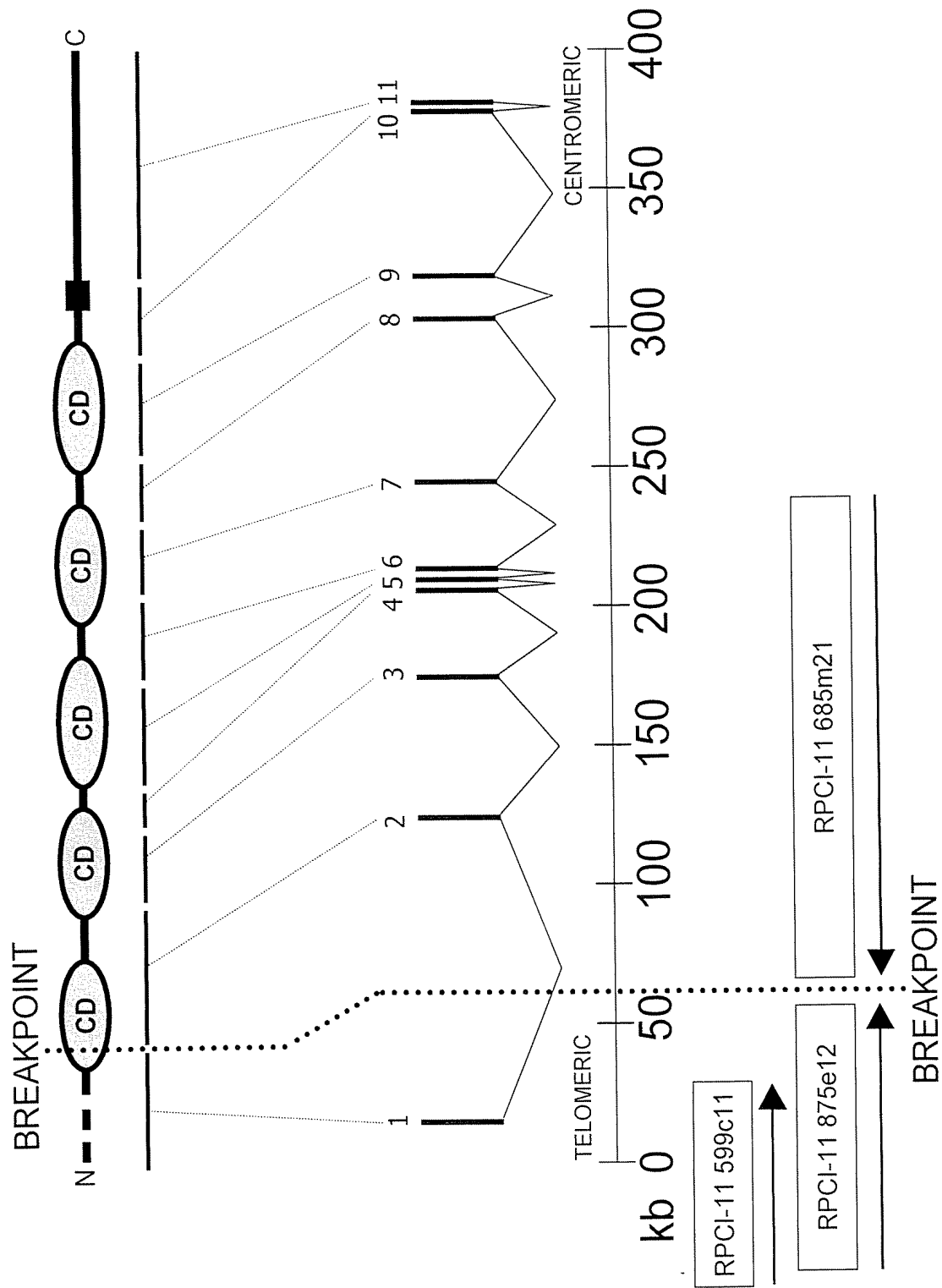


Figure 34



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Figure 35 (SEQ ID NO: 61)

```
1 agccatttgt gaacctggag gcttgacatt cgccagcgca gggccccaca agagaaatth
61 caatgaaaag aaaagccaat ggattgtggt cttagaaaag ctgcttagat gatgtctgth
121 tcccgtgcta tagacacgtg gcagagctgt aagtaaatgc tcggcactgc atgatgaatt
181 ggatggctgc agaccggaga caaaaaaaat aattgtctca ttttcgtggt gatttgctta
241 actgggtgga ccatgccaga acggctagcg gaaatgctct tggatctctg gactccatta
301 ataataattat ggattactct tcccccttgc atttacatgg ctccgatgaa tcagtctcaa
361 gttttaatga gtggatcccc tttggaacta aacagtctgg gtgaagaaca gcgaatthtg
421 aaccgctcca aaagaggctg ggthtggaat caaatgtthg tcctggaaga gththtctgga
481 cctgaaccga ttcttgttgg cgggtacac acagacctgg atcctgggag caaaaaaatc
541 aagtatatcc tatcaggatga tggagctggg accatatttc aaataaatga tgtaactgga
601 gatatccatg ctataaaaag acttgaccgg gaggaagg ctgagtatac ctaacagct
661 caagcagtg actgggagac aagcaaacct ctggagcctc cttctgaatt tattattaaa
721 gttcaagaca tcaatgacaa tgcaccagag tttcttaatg gacctatca tgctactgtg
781 ccagaaatgt ccattthggg tacatctgtc actaacgtca ctgcgaccga cgctgatgac
841 ccagthtatg gaaacagtgc aaagthggth tatagtatat tggaagggca gcctththth
901 tccattgagc ctgaaacagc tattataaaa actgcccttc ccaacatgga cagagaagcc
961 aaggaggagt acctggttgt tatccaagcc aaagatatgg gtggacactc tggthggctg
1021 tctgggacca cgacacttac agtgactctt actgatgtha atgacaatcc tccaaatth
1081 gcacagagcc tgtatcactt ctcagtagcg gaagatgtgg ttcttggcac tgcaatagga
1141 agggatgaag ccaatgatca ggatattggg gaaaatgcac agtcatcata tgatatcatc
1201 gatggagatg gaacagcact ttttgaaatc acttctgatg cccaggccca ggatggcatt
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1381 acagtcaaaa tctgtgthga agatgctgat gagctcccg tcttctcttc accgacttac
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1861 ccagaaatgg tcaacaatcc gaatttcacc atcaagaaaa atgaagataa thccctcagt
1921 atththggca agcataatgg attcaaccgc cagaagcaag aagtctatct thtaccatc
1981 ataatacagt atagtggaaa tcctccactg agcagcacta gcaccttgac aatcagggtc
2041 tgtggctgca gcaatgacgg tgtcgtccag tcttgcaatg tcgaagctta tgtcctthca
2101 attggactca gtatgggctg cthtaattgc atattagcat gcatcattth gctgthtagt
2161 atcgtggtgc tgtthgtaac tctacggcg cataaaaatg aaccattaat tatcaaagat
2221 gatgaagacg ttcgagaaaa catcattcgc tacgatgatg aaggaggagg ggaggaggac
2281 acagaggctt ttgacattgc aactthtaca aatccagatg gaattaatgg atththtacc
2341 cgtaaggata ttaaaccaga thtgagtht atgccaaggc aagggttgc tccagthcca
2401 aatgggtgth atgtcgatga atthtataat gtaaggctgc atgaggcaga taatgatccc
2461 acggccccgc catatgactc cattcagata tatggctatg aaggccgagg gtcagthggt
2521 ggctccctca gctccttgga gtccaccaca tcagactcag accagaatth tgactacctc
2581 agtgactggg gtccccgctt taagagactg ggcgaaactc actctgthtg tgaaagtgc
2641 aaagaaactt gacagthgat tataaataaa tcaactggaac tgagcattct gtaatttht
2701 aggtctactc cctthtagata caaccaatgt ggctatthgt thtagaggca agthtagcac
2761 cagthcatcta taaactcaac cacatththaa gthtgaaaca aaaaaagata ataaataaaa
2821 aaagtatatg ttaggaggtt ataaatcttg tggagtgtga attaagtatg tggagtgtct
2881 agaagthctt ggatattthga taththacct accaccacag acaaagatt
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Figure 36 (SEQ ID NO: 62)

1 MPERLAEMLL DLWTPLIILW ITLPPCIYMA PMNQSQVLMS GSPLELNSLG EEQRILNRSK
61 RGWVWNQMFV LEEFSGPEPI LVGRLHTDLD PGSKKIKYIL SGDAGATIFQ INDVTGDIHA
121 IKRLDREEKA EYTLTAQAVD WETSKPLEPP SEFIKQVDI NDNAPEFLNG PYHATVPEMS
181 ILGTSVTNVT ATDADDPVYG NSAKLVYSIL EGQPYFSIEP ETAIIKTALP NMDREAKEYEY
241 LVVIQAKDMG GHSGGLSGTT TLTVTLTVDN DNPPKFAQSL YHFSVPEDVV LGTAIGRVKA
301 NDQDIGENAO SSYDIIDGDG TALFEITSDA QAQDGIIRLR KPLDFETKKS YTLKVEAANV
361 HIDPRFSGRG PFKDTATVKI VVEDADEPPV FSSPTYLLEV HENAALNSVI GQVTARDPDI
421 TSSPIRFSID RHTDLERQFN INADDGKITL ATPLDRELSV WHNITIIATE IRNHSQISRV
481 PVAIKVLDVN DNAMEFASEY EAFLCENGKP GOVIQTVSAM DKDDPKNGHY FLYSLLPEMV
541 NNPNFTIKKN EDNSLSILAK HNGFNRQKQE VYLLPIIISD SGNPPLSSTS TLTIRVCGCS
601 NDGVVQSCNV EAYVLPIGLS MGALIAILAC IILLLVIVVL FVTLRRHKNE PLIIKDDDEV
661 RENIIRYDDE GGGEEDTEAF DIATLQNPDG INGFLPRKDI KPDLOFMPRQ GLAPVPNGVD
721 VDEFINVRLH EADNDPTAPP YDSIQIYGYE GRGSVAGSLS SLESTSDSD QNFDYLSDWG
781 PRFKRLGELY SVGESDKET

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Figure 37

a) (SEQ ID NO: 63)

MPERLAEMLLDLWTPLIILWITLPPCIYMAPMNQSQVLMSGSPLELNSLGEEQRILNRSKRG
 WVWNQMFVLEEFSGPEPILVGRVLKSVSKLH*

b) (SEQ ID NO: 64/65)

G R G G A A E A P R A G G G R L L R G Q
 3 ggccgcggcggtgcagcagaggcgccctcgggcaggaggaggcggttctgcgagggcag 62
 P E L H T D L D P G S K K I K Y I L S G
 63 cctgagctacacacagacctggatcctgggagcaaaaaaatcaagtatatcctatcaggt 122
 D G A G T I F Q I N D V T G D I H A I K
 123 gatggagctgggaccatatttcaaataaatgatgtaactggagatatccatgctataaaa 182
 R L D R E E K A E Y T L T A Q A V D W E
 183 agacttgaccgggaggaaaaggctgagtataccctaacagctcaagcagtgaggactgggag 242
 T S K P L E P P S E F I I K V Q D I N D
 243 acaagcaaacctctggagcctccttctgaatttattattaaagttcaagacatcaatgac 302
 N A P E F L N G P Y H A T V P E M S I L
 303 aatgcaccagagtttcttaatggaccctatcatgctactgtgccagaaatgtccattttg 362
 G T S V T N V T A T D A D D P V Y G N S
 363 ggtacatctgtcactaacgtcactgacgacctgatgacctggtttatggaaacagt 422
 A K L V Y S I L E G Q P Y F S I E P E T
 423 gcaaagttggtttatagtatattggaagggcagccttatttttccattgagcctgaaaca 482
 A I I K T A L P N M D R E A K E E Y L V
 483 gctattataaaaaactgcccttcccaacatggacagagaagccaaggaggagtacctgggt 542
 V I Q A K D M G G H S G G L S G T T T L
 543 gttatccaagccaaagatatgggtggacactctggtggcctgtctgggaccacgacactt 602
 T V T L T D V N D N P P K F A Q S L Y H
 603 acagtgactcttactgatgttaatgacaatcctccaaaatttgcacagagcctgtatcac 662
 F S V P E D V V L G T A I G R V K A N D
 663 ttctcagtaccggaagatgtggttcttggcactgcaataggaaggggtgaaggccaatgat 722
 Q D I G E N A Q S S Y D I I D G D G T A
 723 caggatatgttgtaaaatgcacagtcacatcatgatcatcgatggagatggaacagca 782
 L F E I T S D A Q A Q D G I I R L R K P
 783 ctttttgaaatcacttctgatgccaggcccaggatggcattataaggctaagaaaacct 842
 L D F E T K K S Y T L K V E A A N V H I
 843 ctggactttgagaccaaaaaatcctatacgctaaaggtagaggcagccaatgtccatatt 902
 D P R F S G R G P F K D T A T V K I V V
 903 gacccacgcttcagtggcagggggccctttaaagacacggcgacagtcaaaatcgtgggt 962
 E D A D E P P V F S S P T Y L L E V H E
 963 gaagatgctgatgagcctccggtcttctcttcaccgacttacctacttgaagttcatgaa 1022
 N A A L N S V I G Q V T A R
 1023 aatgctgctctaaactccgtgattgggcaagtgactgctcgt etc.....